Access DB# 49312

## SEARCH REQUEST FORM

Scientific and Technical Information Center

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Requester's Full Name:		Examiner # :	Date:
Art Unit:	Phone Number 30	Serial Number:	DANCE DICK E MAII
Mail Box and Bldg/Roo	m Location:	Examiner # :	PAPER DISK E-MAIL
******	*****	prioritize searches in order of ne	****
Include the elected species of utility of the invention. Def	r smichires, keywords, synony	d describe as specifically as possible the sub yms, acronyms, and registry numbers, and c special meaning. Give examples or relevar claims, and abstract.	ombine with the concept of
Title of Invention:			
Inventors (please provide	full names):		
Earliest Priority Filing	Date:		
*For Sequence Searches Onlappropriate serial number.	y* Please include all pertinent in	nformation (parent, child, divisional, or issued p	atent numbers) along with the

STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher:	NA Sequence (#)	STN
Searcher Phone #:	AA Sequence (#)	Draiog
Searcher Location:	Structure (#)	Questel:Orbi:
Date Searcher Picked Up	Bibliographic	Dr.Link
Date Completed State	Litigation	Lexis/Nexis
Searcher Prep & Review Time	Fulltext	Sequence Systems
Clencal Prep Time	Patent Family	WWW/Internet
Online Time	Other	Other (specify)

PTO-1590 (1-2000)

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AR1955 Human conne
AR1955 Sequence
111636 Sequence 1
13210 Sequence 1
M92934 Human conne
X78947 H.saptens m
V70060 Sus scrofa
AF000137 Bos tauru
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Catarrhini; Hominidae; Homo.
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Pred. No. 6.4e-131
                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniat,
Mammalla; Eutheria; Primates; Catarrh
(bases 1 to 2075)
Grotendorst,G.R. and Bradham,D.M. Jr.
Connective tissue growth factor(CTGF)
Patent: US 5408040-A 1 18-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Sequence 1 from Patent US 5408040.
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Grotendorst,G.R. and Bradham,D.M. Jr.
Treatment of cell proliferative disorders using antibodies which
bind connective tissue growth factor
Patent: US 578187-A 1 21-JUL-1998;
Location/Qualifiers
1. 2075
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100.0%; Pred. No. 6.4e-131;
Live 0; Mismatches 0;
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                                                                                                                                                                       Location/qualifiers
1. .2075
7. .2075 "Homo sapiens"
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Grotendorst, G.R.
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1 (bases 1 to 2075)
2 (Bardham, D.M.; Igarashi,A., Potter,R.L. and Grotendorst,G.R. Connective tissue growth factor: a cysteine-rich mitogen secreted connective tissue growth factor: a cysteine-rich mitogen secreted by human vascular endothelial cells is related to the SRC-induced immediate early gene product CEF-10
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1 (corendors), G.R. and Bradham, D.M. Jr.
Grotendors, G.R. and connective tissue growth factor
Polynucleotides encoding connective tissue prowth factor
Patent: US 5585270-A 1 17-DEC-1996;
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11ve 0; Mismatches 0;
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Submitted (22-APR-1994) B.S. Oemar, University Hospital Basel, Dept
of Research, Lab of Vascular Research, Hebelstr. 20, 4031 Basel,
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CETGGTVYRSCBSFQSSCKYQCTCLDGAVGCMPLCSMDYRLPSPDCPPFRVKLFGKC
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TRVINNNASCRLEKQSRLCMYRFCEADLEENIKGKKCIRTPKLSKPIKFELSGCTSM
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                                                                                HSCTGF 2312 bp mRNA PRI 1
H.sapiens mRNA for connective tissue growth factor.
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/map="6q23.1"
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Best Local Similarity 100.0%; Pred. No. 6.4e-131;
Matches 510; Conservative 0; Mismatches 0;
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1147 TACTACAGGAAGATGTACGGAGACATGGCA 1176
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                                                                                                                                               connective tissue; growth factor.
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1486. .1487
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Oemar, B.S.
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/translation="MAATGLEPWRAFVLLLALCSRPASGQDCSGQCQCAAGKRRACP
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TRYTNDNASCRLEKQSRLCMYRPCEADLEENIKKGKKCIRTPKISKPVKFELSGCTSV
TRYTRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEVMKKSMMFIKTCACHYNCPGDND
IFESLYYRKMYGDMA
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Harding, P.A. and Brigstock, D.R.
Cloning and sequencing of a porcine connective tissue growth factor
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Sus.
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Sus scrofa connective tissue growth factor (CTGF) mRNA, complete
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181 aggccttgcgaagctgacctggaagagaacattaagaagggcaaaaagtgcatccgtact
                                                                                             Children's Hospital, 700
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
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Submitted (09-SEP-1996) Surgery, Children
Children's Drive, Columbus, OH 43205, USA
Location/Qualifiers
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Harding, P.A. and Brigstock, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="uterus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="CTGF"
206. .1255
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Submitted (17-APR-1997) Internal Medicine I, University of
Submitted (17-APR-1997) Internal Medicine I, University of
Heidelberg, Im Neuenheimer Feld 324, 3.0G, R320 69120, Heidelberg
Location/Qualifiers
1. .2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Ruminantia; Pecora; Bovoidea; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.

1 ( bases 1 to 2330)

1.11iensiek, B., Lińt, Z., Fotsis, T., Schimanski, M., Bierhaus, A., Kanitz, M., Kuuffmann, G., Schweigerer, L., Ziegler, R. and Kanitz, M., Ruffmann, G., Schweigerer, E., Ziegler, R. and Nawroth, P.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                  BTAF000137 2330 bp mRNA MAM 13-AUG-1997
Bos taurus connective tissue growth factor precursor (CTGF) mRNA,
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Liliensiek, B., Lin, Z., Fotsis, T., Schimanski, M., Bierhaus, A.,
Kanitz, M., Kauffmann, G., Schweigerer, L., Ziegler, R. and
Nawroth, P.P.
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                         ;
                               Length 1598;
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus connective tissue growth factor
                                  Score 451.4; DB 7;
Pred. No. 1.2e-114;
0; Mismatches 36;
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   443
                                       88.5%;
92.9%;
                                        Query Match
Best Local Similarity 92.9
Matches 473; Conservative
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AUTHORS
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VERSION
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/LTAINSTALTION="MGATGLGPVRCAFVLLLALCSRPASSODCCSAPCOCPAGPAPRC
/LTAINSTALTION="MGATGLGPVRCAFVLLLALCSRPASSODCCSAPCOCPARDGAP
PAGVSLVLLDGCGCCVCARQLSELCTBENDFOPHREGECOPGSPTNRKIGVCTARGAR
YIFGGTVYQSGESFOSSCKYQCTCLDGSVGCVPLCSVDVRLPSPDCFPRRVKLPGKC
CEBWYSRDEREHTVVGPALARYRLEDYFGPDFMIRANCOVQTTEWSAYSKTGGMGIS
TRYTNDNARCRLENGSRLCMVRPCEADLEBNIKKGKKCIRTPKISKPIRFOLSGCTSM
KTYRAKFFGVCTDGRCCTPHRTTTLPVEFKCPDGEVMKKSMMFINTCACHYNCPGDND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="secreted protein; cysteine-rich member of the CTGF growth factor family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 accetgeoggtggagtteaagtgeoctgaeggegaggteatgaagaagaacatgatgt 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="growth promoting and chemotactic factor for mesenchymal cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                 /function="growth promoting and chemotactic factor for mesenchymal cells"
                                                                                                                                                                                                                                                                                                                                  /note="secreted protein; cysteine-rich member of the
                                                                                                                                                              /product="connective tissue growth factor precursor"
/protein_id="AAB66596.1"
/db_xref="G1:2326194"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 goggettacogactggaagacacgtttggcccagacccaactatgattagagccaactgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2330;
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624 c 588 g 551 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.5%; Score 451.4; DB 7;
92.9%; Pred. No. 1.2e-114;
iive 0; Mismatches 36;
                                  /cell_type="endothelial"
/organism="Bos taurus"
/db_xref="taxon:9913"
/cell_line="BAEC"
                                                 /tissue_type="aorta"
1. .2330
                                                                                                                                                                                                                                                                                               206. .289
/gene="CTGF"
290. .1252
                                                                                                                                                                                                                                                                                                                         290. .1252
/gene="CTGF"
                                                                     /gene="CTGF"
206. .1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 92.9
Matches 473; Conservative
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/translation="MLASVAGPISLALVILALCTRPATGQDCSAQCQCAAEAAPHCPA
GVSLVLDGCGCCRVCAKQLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAKDGAPC
VFGGSYVRSGESFQSSCKXQCTCLDGAVGCPLCSMDVRLPSPDCPFPRRKLPGKCC
KEWVCRFTAVGAAT KLEDFTEPTPMRANCLVQTTFWSACSKTCGMGIST
RVTNDMTFCRLEKQSRLCMVRPCEADLEBNIKKGKKCIRTPKIAKPVKFELSGCTSVK
TYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEIMKKNMMFIKTCACHYNCPGDNDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2267)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M70642.1 GI:193315 cysteine-rich protein; growth factor-inducible gene. Mus musculus (sub_species domesticus) liver/kidney cDNA to mRNA. Mus musculus
                                                                                                                                         361 accetgocogitggagitcaagitgcoctgacoggcgaggicaigaagaagaacaigaigitc 420
                                                                                                                                                                                                                                                                                                                                                   421 atcaagacctgtgcctgccattacaactgtcccggagacaatgacatctttgaatcgctg 480
     863 CGGCTTACCAATGACAACGCTTTCTGCAGACTGGAGAAGCAGAGCCGCCTCTGCATGGTC 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ryseck, R.-P., MacDonald-Bravo, H., Mattei, M.-G. and Bravo, R. Structure, mapping and expression of fisp-12, a growth factor inducible gene encoding a secreted cysteine-rich protein (2011 Growth Differ. 2, 225-233 (1991)
                                                                                                                   241 cccaaaatctccaagcctatcaagtttgagctttctggctgcaccagcatgaagacatac
                                                                                                                                                                                                cgagctaaattctgtggagtatgtaccgacggccgatgctgcacccccacagaaccacc
                                                                                                                                                                                                                                                                                                DB 94; Length 2267;
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Mouse FISP-12 protein (fisp-12) mRNA, complete cds.
M70642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sub_species="domesticus"
/db_xref="taxon:10090"
/tissue_type="liver/kidney"
//map="A3-81"
138. .2230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="FISP-12 protein"
/protein_id="AAA37628.1"
/db_xref="G1:193316"
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    .2267
    /organism="Mus musculus"

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/gene="fisp-12"
138. .110.
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/gene="fisp-12"
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MUSFISP12B
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/protein_id="AAAA8756.1"
/protein_id="AAAA8756.1"
/protein_id="AAAA8756.1"
/protein_id="GI:3317898"
/translation="MARATGLSPWCAFFVLLIALCSRPASGODCSGOCOCAAGKRRACP
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CVFGGTVYRSGESFGSSCKYQCTCLDGAVGCPPLCSMUVRLBSPDCPFPRRKLPGKC
CEGWVCDEPKDHTVGPALAAYRLEDTFGPDPTMMRANCLVQTTEWSACSKTCGMGIS
TRYTNDNARCRLEAGSRLCAWVRCEADLEGNIKKGKKCIRTPKISKPVKFELGGGCTSV
KTYRAKRCGVCTDGRCCTPHRTTLEPVEFKCPDGEVMKKSMMFIKTCACHYNCPGDND
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                                                                                                                                                                                                                                                                                                                                                                                   Purification and characterization of novel heparin-binding growth factors in uterine secretory fluids. Identification as heparin-regulated Mr 10,000 forms of connective tissue growth
                                                                                                                                                                                                                                                                                            Euteleostomi;
Sus.
                                                                                                                                   SSU83916 1496 bp mRNA MAM 12-AUG-1997
Sus scrofa connective tissue growth factor (CTGF) mRNA, complete
                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 1496)
Brigstock, D.R., Steffen, C.L., Kim, G.Y., Vegunta, R.K., Diehl, J.R. and Harding, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cgggttaccaatgacaacgcctcctgcaggctagagaagcagagccgcctgtgcatggtc 180
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/note="N-terminally G/C rich; contains 38 cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (06-JAN-1997) Surgery, Children's Hospital, 700 Children's Drive, Columbus, OH 43205, USA Location/Qualifiers
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
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Pred. No. 9e-114;
0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 272 (32), 20275-20282 (1997)

    1496
/organism="Sus scrofa"
/db_xref="taxon:9823"

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1. .1496
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Harding, P.A. and Brigstock, D.R.
Direct Submission
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206. .1255
/gene="CTGF"
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U83916.1
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SSU83916
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FESLYYRKMYGDMA"
204. .278
279. .1247
2291. .2296
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90.8%;
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Matches 462; Conserv
                                                                                               589
                       sig_peptide
mat_peptide
polyA_signal
polyA_site
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AUTHORS
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/db_xref="ad1:2013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-APR-1993
                                                                                                                                                                                                                                                                                                                                                             ;
0
                                    Pred. No. 9e-110;
0; Mismatches 47; Indels
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91229699
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/organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="AKR-28"
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Hansforming growth factor-beta.
Hus musculus cDNA to mRNA.
Mus musculus
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Mouse mRNA sequence.
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Direct Submission
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Submitted (01-FEB-1999) to the DDBJ/EMBL/GenBank Laboratories,JT
Ratsunari Tezuka, pharmaceutical Frontier Research Laboratories,JT
Ratsunari Tezuka, pharmaceutical Frontier
Tec, Devision of Molecular Immunology: 13-2, Fukuura
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Rattus norvegicus mRNA for connective tissue growth factor,
                           Gaps
Score 433.8; DB 94; Length 2330;
Pred. No. 9e-110;
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Tecuka, K. and Tamatani, T.
Tecuka, K. and Tamatani, T.
Ratus norvegious connective tissue growth factor
Tecuka, K. and Tamatani, T.
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Rattus norvegicus
Rattus norvegicus
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1-chome,kanagawa-ku, Yokohama, Kanagawa 236-0004, Japan
(E-mail:katsunari.tezuka@ims.jti.co.jp, Tel:81-45-786-7693,
Fax:81-45-786-7692)
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Pred. No. 9e-110;
0; Mismatches 47; Indels 0;
                                                                                                     /product="connective tissue growth factor"
/protein_id="BAA82125.1"
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                                             /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/cell_line="NRK-49F"
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AF120275 2345 bp mRNA ROD 12-APR-2000 Rattus norvegicus connective tissue growth factor mRNA, complete

GI:5070343

AF120275 AF120275.1

DEFINITION

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FGGSVYRSGESFQSSCKYQCTCLDGAVGCVPLCSMDVRLPSPDCPFPRVKLPGKCCE
WCDEPKDFYVGPALABY RLEDTFGPDPTMANCLVQTTWBAGSKYCGMG1STR
VNDNYFCRLEKQSRLCMVRPCFADLEBNIKKGKKCITRPKTAKPVKFELSGCTSVKY
YRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEIMKKNMMFIKTCACHYNCPGDNDIF
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VSLVLDGCGCCRVCAKQLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAKDGAPCV
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Street,
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                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-JAN-1999) Cardiovascular and Metabolic Diseases, Pfizer Central Research, Eastern Point Road, Groton, CT 06340,
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                                                                                                                        Xu,J., Smock,S.L., Śafadi,F.F., Rosenzweig,A.B., Odgren,P.R., Marks,S.C. Jr., Owen,T.A. and Popoff,S.N. Cloning the full-length cDNA for rat connective tissue growth factor: implications for skeletal development 20145935 10chm. 77 (1), 103-115 (2000)
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Xu,J., Rosenzweig,A.B., Safadi,F.F. and Popoff,S.N.
Direct Submission
Submitted (09-JUN-1999) Department of Anatomy and Cell
Temple University School of Medicine, 3400 North Broad
Philadelphia, PA 19140, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="connective tissue growth factor"
/protein_id="AAD39132.1"
/db_xref="G1:5070344"
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/db_xref="taxon:10116"
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Odgren, P.R. and Marks, S.C. Jr.
Direct Submission
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Smock, S.L. and Owen, T.A.
Direct Submission
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90.8%;
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Matches 462; Conservative
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Gates, P.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission Direct Submission Span D., Institute of Physiology, Submitted (19-JAN-2001) Gygi D., Institute 190, 8057, SWITZERLAND University of Zurich, Winterthurerstrasse 190, 8057, SWITZERLAND Location Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 7.8e-100;
0; Mismatches 70; Indels (
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l (bases 1 to 1585)
Cash,D.E., Gates,P.B., Imokawa,Y. and Brockes,J.P.
Gates,Teation of newt connective tissue growth factor as a target of retinoid regulation in limb blastemal cells
Gene 222 (1), 119-124 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                NVI271167 1585 bp mRNA vRT 14-JAN-2000 NOTD71167 1585 bp mRNA for connective tissue growth factor (ctgf gene).
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Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
Notophthalmus.
                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (11-JRN-2000) Gates P.B., Biochemistry, University
Submitted (11-JRN-2000) Gates P.B., Biochemistry, University
College London, Gower Street London, WClE 6BT, UNITED KINGDOM
College Location/Qualifiers
                                                                                                                                                                                                                                 121 cgggttaccaatgacaacgcctcctgcaggctagagaagcagagccgcctgtgcatggtc 180
                 181 aggccttgcgaagctgacctggaagagaacattaagaagggcaaaaagtgcatccgtact 240
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137. 1180
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YRAKFGGVCTDGRCCTPHRTATLPVEFKCPDGEVMKKMMFIKTCACHYNCPGDNDIF
ESMYYRKMYGDMA"
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454 g 428 c 383 BASE COUNT ORIGIN

ö Gaps ó DB 8; Length 1585; Score 381; DB 8; Length 158 Pred. No. 4e-95; 0; Mismatches 80; Indels Ouery Match
Best Local Similarity 84.3%;
Matches 429; Conservative ç

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Bovine mammary tis Polynucleotide RTP Mouse connective t Rat connective tis Chicken nov coding

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Human; connective tissue growth factor; CTGF; mitogen; antibody; liver; fibroproliferative disease; scleroderma; fibrosis; kidney; arthritis; hypertropic scarring; atherosclerosis; diabetic nephropathy; retinopathy; hypertension; cardiovascular disorder; wound healing; bone repair; ss.
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                                                           This sequence represents a partial coding sequence for the human connective tissue growth factor (CTGF) polypeptide which has mitogenic connective tissue growth factor (CTGF) polypeptide which has mitogenic activity. The sequence spans the open reading frame covering exons 2 and activity. The sequence (AAA11280). The protein can be used to raise antibodies which specifically bind to CTFG and are used to treat a cTGF-associated disease or disorder, e.g. a fibropholiferative fibrosis, alver fibrosis, activities, scleroderma, pulmonary fibrosis, liver fibrosis, arthritis, hypertropic scarring, ratherosclerosis, diabetic nephropathy and retinopathy, hypertension, kidney disorders, anglogenesis-related disorders, skin fibrotic disorders, and cardiovascular disorders. The protein is also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps.
New fragment of connective tissue growth factor (CTGF) polypeptide having mitogenic activity, useful in wound healing, bone and tissue
                                                                                                                                                                                                                                100.0%; Score 510; DB 21; Length 1415; 100.0%; Pred. No. 8.9e-145; Indels 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                      Sequence 1415 BP; 403 A; 299 C; 329 G; 384 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tactacaggaagatgtacggagacatggca 510
                                                                                                                                                                                      in wound healing, bone and tissue repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Connective tissue growth factor CDNA.
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ID AAT04226 standard; cDNA; 2075
                                                   Disclosure; Fig 3; 71pp; English.
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                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.º
Matches 510; Conservative
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                                         repair -
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847 aggccttgcgaagctgacctggaagagaacattaagaagggcaaaaagtgcatccgtact 906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 aggeettgegaagetgaeetggaagagaacattaagaagggeaaaagtgeateegtaet
                                                                                                                                                                                                                                                                                                                                                                           A cDNA clone (AAT04226), designated DB60R32, codes for human connective tissue growth factor (CTGF) (AAR79964), a protein that connective tissue growth factor and chemotactic activity for connective tissue cells and which binds to the platelet-derived growth factor cells and which binds to the platelet-derived growth factor unbilical vain endothelial cell cDNA in vector lambda gtll by umbilical vein endothelial cell cDNA in vector lambda gtll by careening with an anti-PDE antibody. The cDNA is useful for screening with an anti-PDE antibody. The cDNA is useful for ircombinant CTGF on in the design of antisense or produce on contracts used to treat disorders associated with results of the constructs used to treat disorders associated with overgrowth of tissue cells, such as cancer, fibrotic diseases
                                                                                                                                                                                                                                                                                                       New connective tissue growth factor - used to develop prods. for wound healing and for diagnosis and therapy of cell proliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
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Connective tissue growth factor; CTGF; wound healing; vulnerary; cell proliferation; cancer; fibrosis; atherosclerosis; diagnosis therapy; mitogen; SS.
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100.0%; Pred. No. 1.1e-144;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                              Example 5; Column 15-18; 12pp; English.
                                                                              Location/Qualifiers
130..1179
/*tag= a
                                                                                                                                                                                                                                                               Grotendorst GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 510; Conservative
                                                                                                                                                                                                               93US-0167628
                                                                                                                                                                                                    91US-0752427
                                                                                                                                                                              91US-0752427
                                                                                                                                                                                                                                     (UYSF-) UNIV SOUTH FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and atherosclerosis
                                                                                                                                                                                                                                                                                     WPI; 1995-161147/21.
P-PSDB; AAR79964.
                                                                                                                                                                                                       30-AUG-1991;
14-DEC-1993;
                                                                                                                                                                                   30-AUG-1991;
                                                                                                                                                                                                                                                                   Bradham DM,
                                                                                                                                                            18-APR-1995.
                                                                Homo sapiens
                                                                                                                                       US5408040-A
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Length 2075;

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Local Similarity 100. es 510; Conservative
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  Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A cDNA clone (AAT45360) codes for novel human connective tissue growth factor (CTGF) (AAW09089), a PDGF-immunorelated protein that may play a significant role in the normal development, growth and repair of human tissue and which probaly functions as a growth factor in wound healing. CTGF may be involved in diseases in which there is an overgrowth of connective tissue cells, such as cancer, tumour formation and growth, fibrotic diseases (e.g. pulmonary fibrosis, kidney fibrosis, glaucoma) and atherosclerosis. The cDNA clone was isolated from a HUVEC cDNA library using anti-PDGF antibody. CTGF nuclest acids can be used for recombinant prodn. of CTGF and as probes to detect CTGF mRNA. CTGF genomic DNA (AAT58534) has also been isolated. A proliferative disorder may be treated using e.g.
                      1146
967 cgagctaaattctgtggagtatgtaccgacggccgatgctgcacccccacagaaccacc 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Connective tissue growth factor coding sequence and protein - used in the treatment of proliferative disorders and to accelerate wound
                                                                                                                                                                                                                                                                                                                        Connective tissue growth factor; CTGF; mitogen; cell proliferation; wound healing; cancer; tumour; fibrosis; glaucoma; atherosclerosis; diagnosis; therapy; antisense; triple helix; ribozyme; ss.
                                                                                        421 atcaagacctgtgcctgccattacaactgtcccggagacaatgacatctttgaatcgctg
                                                                                                                                                                                                                                                                                                 connective tissue growth factor cDNA.
                                                                                                                                          481 tactacaggaagatgtacggagacatggca 510
                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
130..1179
/*tag= a
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                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                    AAT45360 standard; cDNA; 2075
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                                                                                                                                                                                                                                                                      (first entry)
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P-PSDB; AAW09089.
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                                                                                                                                                                                                                                                                      26-APR-1997
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Sequence 2075 BP; 491 A; 558 C; 546 G; 480 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                       967 cgagctaaattctgtggagtatgtaccgacggccgatgctgcacccccacagaaccacc 1026
                                                                                                                                                                421 atcaagacctgtgcctgccattacaactgtcccggagacaatgacatctttgaatcgctg 480
                                                                                                           61 ctggtccagaccacagagtggagcgcctgttccaagacctgtgggatgggcatctccacc 120
                                                                                                                           847 aggcettgegaagetgacetggaagagaacattaagaagggeaaaagtgeateegtaet 906
                                                                      Gaps
                                                       1 gcggcttaccgactggaagacacgtttggcccagacccaactatgattagagccaactgc
                                                                                                                                                                                                                     181 aggccttgcgaagctgacctggaagagaacattaagaagggcaaaaagtgcatccgtact
                                                                                                                                                                                                                                                                                                                                   cgagctaaattctgtggagtatgtaccgacggccgatgctgcacccccacagaaccacc
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                              Indels
            1.1e-144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Connective tissue growth factor coding sequence.
                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 tactacaggaagatgtacggagacatggca 510
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130..1179
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100.0%;
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93US-0167628.
95US-0386680.
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14-DEC-1993;
10-FEB-1995;
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This sequence represents the cDNA encoding the human connective tissue craft factor (CTGE). CTGF is related immunologically and biologically active factor (CTGE). Dut is encoded by an unrelated growth factor (PDGF), but is encoded by an unrelated compared growth factor (PDGF), but is encoded by an unrelated compared growth factor (PDGF), but is encoded by an unrelated compared is thought to play a significant role in the normal case of gene was isolated by screening a cDNA library from human umbilical development, growth, and repair of human tissue, similarly to PDGF. This capture modothelial (HUVE) cells with anti-PDGF antibodies. CTGF may be used to accelerate wound healing. Also, elevated levels of CTGF may be used to accelerate wound healing. Also, elevated levels of CTGF may be used to accelerate wound also serve as assay reagents). All these diseases can be treated with reagents sective with CTGF, such these diseases can be treated with reagents. Antisense of these diseases can be treated with reagents. Antisense calls and ribozymes could also be used to inhibit CTGFs in production. The advantage with using CTGF is that it is more stable, can effect in wound healing. This is believed to be due to the contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding connective tissue growth factor - useful
for accelerating wound healing, also for diagnosis and treatment of
proliferative disease
                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 510; DB 18; Length 2075; 100.0%; Pred. No. 1.1e-144; ative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                      Sequence 2075 BP; 491 A; 558 C; 546 G; 480 T; 0 other;
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                       Grotendorst GR;
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
(UYSF-) UNIV SOUTH FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 510; Conserv
                                                WPI; 1997-051180/05.
p-PSDB; AAW11302.
                                                                                                                                                                                                                                                                                                                                                high Cys content.
                              Bradham .DM,
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A method has been developed for ameliorating a cell proliferative disorder associated with connective tissue growth factor (CTGF). The method comprises the administration of an antibody or lus fragment that binds to CTGF and not to platelet-derived growth factor (PDGF), to the site of the disorder. CTGF is related immunologically and biologically to PDGF. The present sequence encodes CTGF. The method is used to treat conditions involving the overgrowth of connective tissue cells such as cancer, atherosclerosis and other fibrotic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cgggttaccaatgacaacgcctcctgcaggctagagaagcagacgcctgtgcatggtc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; connective tissue growth factor; CTGF; PDGF; diagnosis; cancer; platelet derived growth factor; ameliorating cell proliferative disorder; atherosclerosis; fibrotic disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 geggettacegaetggaagacaegtttggccagacceaactatgattagagceaactgc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ameliorating cell proliferative disorder associated with connective tissue growth factor - comprises the administration of an antibody which binds to connective tissue growth factor and not to platelet-derived growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2075;
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                                                                                                                                                                                                                                     /*tag* a /product* "connective tissue growth factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2075 BP; 491 A; 558 C; 546 G; 480 T; 0 other:
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100.0%; Pred. No. 1.1e-144;
tive 0; Mismatches 0;
                                                                                                                       Human connective tissue growth factor encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 6; Column 15-18; 11pp; English.
tactacaggaagatgtacggagacatggca 1176
                                                                                                                                                                                                                     Location/Qualifiers
130..1179
                                                             ВР
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93US-0167628.
96US-0712302.
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Best Local Similarity 100.0
Matches 510; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Grotendorst GR;
                                                          AAV38085 standard; cDNA; 2075
                                                                                                                                                                                                                                                                                                                           96US-0712302
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                                                                                                          (first entry)
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p-PSDB; AAW62084.
                                                                                                                                                                                                                                                                                                                                                      30-AUG-1991;
14-DEC-1993;
11-SEP-1996;
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                                                                                                                 15-SEP-1998
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                                                                                          AAV38085;
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Sequence 2075 BP; 491 A; 558 C; 546 G; 480 T; 0 other;
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accetgccggtggagttcaagtgccctgacggcgaggtcatgaagaagaacatgatgttc
                                                                      aggccttgcgaagctgacctggaagagaacattaagaagggcaaaaagtgcatccgtact
                                                                                                                                                                                                       cccaaaaatctccaagcctatcaagtttgagctttctggctgcaccagcatgaagacatac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting cell proliferative disorders such as fibrotic disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encodes the human connective tissue growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGF; connective tissue growth factor; human; fibrotic disease; cell proliferative disorder; atherosclerosis; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human connective tissue growth factor coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1147 tactacaggaagatgtacggagacatggca 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Column 15-18; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tactacaggaagatgtacggagacatggca
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96US-0712302.
97US-0880031.
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11-SEP-1996;
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                                                                                                                                                                                                                                                                              nephrotropic; ophthalmological; hypotensive; cardiant; tranquilizer; vulnerary; antiinflammatory; human; connective tissue growth factor; CTGF; extracellular matrix synthesis; collagen synthesis; antibody; myofibroblast differentiation; antisense; fibroproliferative disease;
                                 Gaps
                                                              9
                                                                                                                                                                                                                                                                                                                                                             cccaaaatctccaagcctatcaagtttgagctttctggctgcaccagcatgaagacatac
                                                               1 geggettacegaetggaagacaegtttggeecagaeecaaetatgattagageeaaetge
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Length 2075;
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                               Indels
100.0%; Score 510; DB 20;
100.0%; Pred. No. 1.1e-144;
ive 0; Mismatches 0;
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98US-0112241
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 Query Match 100.
Best Local Similarity 100.
Matches 510; Conservative
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14-DEC-1998;
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Key
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                                                                  RESULT
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                                                                                                                                                                                   This sequence represents the full coding sequence for the human connective tissue growth factor (CTGF) polypeptide having the ability connective tissue growth factor (CTGF) polypeptide having the ability and connective extracellular matrix synthesis, collaqen synthesis and/or to induce extracellular matrix synthesis, collaqen synthesis and control or mycibroblast differentiation. The invention risk be used to raise control or sequence and the coding sequence can be used to raise sequence can be used in a method to treat a CTGF associated disease or ollsorder such as a fibroproliferative disease or disorder, especially sequence can be used in a method to treat a CTGF associated disease or cliptosis, arthritis, hypertropic scarring, atheroscierosis, liver collogenesis-related disorders, soleroderma, pinnonary fibrosis, liver control of the disease or disorders, and list of disease or disorders, and list disease or disorders, and list disease or disorders, and list diseases caused by vascular endothelial cell and fibrosis of organs), diseases caused by vascular endothelial cell and fibrosis of organs), diseases caused by vascular endothelial cell control of disease, crohn's disease, joint inflammation, interstitial disease, con in the control of the control of disease, crohn's disease, joint inflammation, interstitial disease,
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                                                                                    Fragment of connective tissue growth factor, useful for treating fibroproliferative diseases or disorders, including kidney fibrosis, scleroderma, arthrilis, hypertropic scarring, atherosclerosis, diabetic nephropathy and retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gegettacegactggaagacacgtttggcccagacccaactatgattagagccaactgc 60
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100.0%; Score 510; DB 21; Length 2075;
Best Local Similarity 100.0%; Pred. No. 1.1e-144;
Matches 510; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2075 BP; 491 A; 558 C; 546 G; 480 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease, Crohn's disease, joint inflammation, in
dermatological diseases, diabetes, and keloids.
                                                                                                                                                                        Disclosure; Fig 3A-B; 74pp; English.
                                                                WPI; 2000-431565/37.
P-PSDB; AAY92939.
                                        Grotendorst GR;
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This sequence represents the full length coding sequence for the human connective tissue growth factor (CTGF) polypeptide which has mitogenic connective tissue growth factor (CTGF) polypeptide which specifically activity. The protein can be used to traise antibodies which specifically e.g. a fibropioliferative disease/disorder such as kidney fibrosis, e.g. a fibropioliferative disease/disorder such as kidney fibrosis, scleroderma, pulmonary fibrosis, liver fibrosis, arthritis, hypertropic scarring, atherosclerosis, diabetic nephropathy and retinopathy in hypertension, kidney disorders, angiogenesis-related disorders, sin hypertension, kidney disorders, and cardiovascular disorders. The protein is also fibrotic disorders, and cardiovascular disorders. The protein is also useful in wound healing, bone and tissue repair.
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                                                                                                                                                                                                                                                                                                       Human; connective tissue growth factor; CTGF; mitogen; antibody; liver; fibroproliferative disease; scleroderma; fibrosis; kidney; arthritis; hypertropic scarring; atherosclerosis; diabetic nephropathy; retinopathy; hypertropic scarring; atherosclerosis; wound healing; bone repair; ss. hypertension; cardiovascular disorder; wound healing; bone repair; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New fragment of connective tissue growth factor (CTGF) polypeptide having mitogenic activity, useful in wound healing, bone and tissue repair -
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/product= "connective tissue growth factor"
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100.0%; Pred. No. 1.1e-144;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                   Human connective tissue growth factor cDNA.
Disclosure; Fig 2A-B; 71pp; English.
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98US-0112241.
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P-PSDB; AAY92940.
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Matches 510;
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                                                                                                      cccaaaaatctccaagcctatcaagtttgagctttctggctgcaccagcatgaagacatac
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                           cgggttaccaatgacaacgcctcctgcaggctagagaagcagagccgcctgtgcatggtc
                                           cgggttaccaatgacaacgcctcctgcaggctagaagaagcagagccgcctgtgcatggtc
                                                             aggccttgcgaagctgaacctggaagaagaacattaagaagggcaaaaagtgcatccgtact
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                                                                                                                                                                                                                                                                                                                                                                       mitogenic; chemotactic; tissue development; growth; repair; wound healing; vulnerary; diagnostic agent; cellular proliferation disorder; ss.
                                                                                                                                                                                                                                                                                                                                                Human connective tissue growth factor (CTGF) cDNA
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30-AUG-1991;
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Claim 9; Column 15-18; 11pp; English

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human connective tissue growth factor (CTGF; AAB60664), involving transforming a prokaryotic or eukaryotic host cell with an expression construct comprising the CTGF cDNA sequence (AAF59954) or a fragment thereof, and culturing the host cell under conditions suitable for the expression of CTGF. CTGF is a mitogen and chemotactic agent for connective tissue cells and plays a significant role in normal development, growth and repair of human tissues. It is useful as a therapeutic for accelerating wound healing and promoting normal healing mechanisms and may therefore be used in the treatment of e.g., burns. CTGF is also useful as a diagnostic reagent for diagnosing pathological states in a patient suspected of having a disease characterised by disorder of cellular proliferation. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1087 atcaagacctgtgcctgccattacaactgtcccggagacaatgacatctttgaatcgctg 1146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cgagetaaattetgtggagtatgtaccgacggecgatgetgeacececeacagaaceace 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    667 geggettacegaetggaagacaegtttggeecagaeceaactatgattagageeaactge 726
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platelet-derived growth factor; transforming growth factor-beta;
TGF-beta; mitogenic; proliferative; chemotactic; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2075;
                                                                                                                                                                                                                                                                                                                                                         Sequence 2075 BP; 491 A; 558 C; 546 G; 480 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 510; DB 22; Best Local Similarity 100.0%; Pred. No. 1.1e-144; Matches 510; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                            CDNA encoding human CTGF
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This cDNA clone codes for murine Fispl2 (see AAW35731), an extracellular matrix signalling molecule (ECM) that exhibits extracellular matrix signalling molecule (ECM) that exhibits structural similarity to (2yf61 (see AAW35730) and which, like structural similarity to (2yf61 (see AAW35730) and which, like Cyrf61, influences cell adhesion, proliferation and migration. Cyrf61, influences cell adhesion, proliferation and migration. Cyrf61 (see Fispl2 polymolectides can be used for the production of factors. Fispl2 polymolectides can be used for the production of Fispl2 polypeptides by recombinant methods. Polypeptide of compositions are provided that comprise mammalian ECM signalling compositions peptide fragments, inhibitory peptides capable of interacting with receptors for ECM signalling molecules, and interacting with receptors for ECM signalling molecules, and commandian ECM signalling molecules to screen for, and/or modulate
                                                                                                                                                                       1027 acctgccggtggagttcaagtgccctgacggcgaggtcatgaagaagaacatgatgttc 1086
                                  361 accetgccggtggagttcaagtgccctgacggcgaggtcatgaagaagaacatgatgt 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated and purified cysteine rich protein 61, Cyr61 - useful to modulate e.g. haematostasis, induce wound healing, promote organ regeneration etc
907 cccaaaatctccaagcctatcaagtttgagcttctggctgcaccagcatgaagacatac 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fispl2; cysteine rich protein; mouse; Cyr61; extracellular matrix signalling molecule; cell adhesion; cell proliferation; angiogenesis; chrondrogenesis; coll migration; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 113-114; 133pp; English.
                                                                                                                                                                                                                                                         Location/Qualifiers
138..1284
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                 AAT94700 standard; cDNA; 2267 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-470875/43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW35731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine Fisp12 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT94700;
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                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to methods of accelerating wound healing in a contact. One method involves contacting the site of the wound with a patient. One method involves contacting the site of the wound with a composition comprising purified connective tissue growth factor to stimulate step production of CTGF in vivo. Another method involves cimulates the production of CTGF in vivo. Another method involves stimulating the growth of connective tissue cells by contacting the cells with CTGF or an active fragment thereof. The produced by cells with CTGF or an active fragment thereof connective tissue cells with CTGF or and is mitogenic and chemotactic for connective tissue cells. It has biologically similar activity to PDGF (platelet-derived site of a wound, and is also immunologically related to it, but it is cells. It has biologically similar activity to PDGF (platelet-derived the product of a distinct gene. CTGF is useful for accelerating wound cells. It may be stimulating the growth of connective tissue cells. CTGF, or protease degradation than PDGF and other growth factors known to be its functional fragments, is more stable and less susceptible to involved in wound healing. The present sequence represents CDNA connecting human CTGF which was isolated and cloned in the centering of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Accelerating wound healing or stimulating growth of connective tissue cells involves contacting the site of a wound or cells with a composition comprising purified connective tissue growth factor and transforming growth factor beta
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100.0%; Score 510; DB 22; Length 2075;
Best Local Similarity 100.0%; Pred. No. 1.1e-144;
Matches 510; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2075 BP; 491 A; 558 C; 546 G; 480 T; 0 other;
                                                         vulnerary; endothelial cell; fibroblast; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Column 15-18; 11pp; English.
                                                                                                                                                                                                                                          93US-0167628.
95US-0386680.
96US-0712302.
91US-0752427.
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                                                                                                                                                                                                                                                                                                                              (UYSF-) UNIV SOUTH FLORIDA.
                                                                                                                                                                                                        98US-0097179
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                                                                                                                                                                                                               12-JUN-1998;
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10-FEB-1995;
                                                                                                                                                                                                                                                                                                     30-AUG-1991;
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                                                                                                              Homo sapiens
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91US-0642991.
92US-0816270.
                                                    WPI; 1992-243508/30.
                                                            P-PSDB; AAR25565
 18-JAN-1991;
10-JAN-1992;
                                      Brunner AM,
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                                                                                                                                                                            240
                                                                                                                                                                                                                                      301 cgagctaaattctgtggagtatgtaccgacggccgatgctgcacccccacagaaccacc 360
                                                                                                                cgggttaccaatgacaacgcctcctgcaggctagagaagcagagccgcctgtgcatggtc 180
                                                                                                                                                                                           911
                                                                                                                                                                                                         241 cccaaaatctccaagcctatcaagtttgagctttctggctgcaccagcatgaagacatac 300
                                                                                 851
                                                                    Gaps
                                                                                                                                                    181 aggoottgogaagotgacotggaagagaacattaagaagggoaaaaagtgoatoogtact
                                                                                                                                                                                    Transforming growth factor beta; induced; CEF-10; v-src; chicken; embryo; fibroblasts; TGF-beta; ss.
disorders associated with angiogenesis, chondrogenesis and oncogenesis; ex vivo methods for using ECM signalling molecules to prepare blood products are also provided.
                                                    Length 2267;
                                                                   .;
0
                                                                   Indels
                              Sequence 2267 BP; 570 A; 568 C; 582 G; 547 T; 0 other;
                                                    Score 433.8; DB 18;
Pred. No. 1.3e-121;
0; Mismatches 47; ]
                                                                                                                                                                                                                                                                                                                                        481 tactacaggaagatgtacggagacatggc 509
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204..1247
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                                                    85.1%;
ilarity 90.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene for beta-IG-M2
                                                                                                                                                                                                                                                                                                                                                                                     AAQ26422 standard;
                                                    Query Match
Best Local Similarity
Matches 462; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                                                                                                                                                                    The DNA encoding mouse beta-IG-M2 was obtd. from AKR-2B mouse cells induced with TGF-betal and cyclohexamide. Poly RNA extracted from these cells was used to create a cDNA library which was screened using two probes. The probes were prepd. from untreated AKR-2B mRNA and AKR-2B mRNA from cells treated with cyclohexamide and TGF-betal. Hybridising colonies were isolated and two clones (beta-IG-M1 and beta-IG-M2) were then sequenced. The DNA encodes proteins that have a 80 and 50 percent homology respectively with the CEF-10 proteins encoded by TGF-beta induced dense mibryo fibroblasts. The proteins encoded by TGF-beta induced genes are likely to be involved in mediation of the biological effects of TGF-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             858 cgagttaccaatgacaataccttctgcagactggagaagcagagccgcctctgcatggtc 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            738 gctgcctaccgactggaagacacatttggcccagacccaactatgatgcgagccaactgc 797
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                                                                                                                                                                                                TGF-beta induced gene family – encodes proteins involved in growth and differentiation effects of TGF-beta-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.1%; Score 433.8; DB 1
90.8%; Pred. No. 1.4e-121
tive 0; Mismatches 47
                                                         Purchio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  relating to cell growth and differentiation
See also AAQ26421.
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                                                      Neubauer MG,
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                                                                                                                                                                                                                                                                                       Claim 7; Fig 2; 35pp; English
(BRIM ) BRISTOL-MYERS SQUIBB
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Best Local Similarity 90.8
Matches 462; Conservative
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06-NOV-1998;
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                                                                                                                                                                                                                                                     21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                               Rattus sp
                                                                                                                                                                                                                                 AAA15477;
                                                                                                                                                                                    RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAX90020 to AAX90029 encode monoclonal antibodies which react with human connective tissue growth factor (CTGF). AAY24369 to AAY24378 represent connective tissue growth factor (CTGF). AAY24369 to AAY24378 represent prese monoclonal antibodies. The antibodies are useful in the diagnosis, prevention and treatment of cell proliferation disorders in which CTGF is implicated, including fibrosis of lung, kidney, liver and other tissues; liver cirrhosis; nephritis; skin ulcers and keloid; rheumatoid arthritis; rheumatic vascular inflammation; hepatitis; and cancer. The present sequence encodes rat CTGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctggtccagaccacagagtggagcgcctgttccaagacctgtgggatgggcatctccac 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     804 ctggtccagaccacagagtggagcgcctgttctaagacctgtgggatgggcatctccacc 863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 gcggcttaccgactggaagacacgtttggcccagacccaactatgattagagccaactgc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                              Human: monoclonal antibody; connective tissue growth factor; CTGF;
cell proliferation disorder; fibrosis; liver cirrhosis; nephritis;
skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer;
rheumatic vascular inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 85.1%; Score 433.8; DB 20; Length 2338; Local Similarity 90.8%; Pred. No. 1.4e-121; Abs. 462; Conservative 0; Mismatches 47; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                        New monoclonal antibody reactive with connective tissue growth factor useful in the treatment of cell proliferation disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2338 BP; 579 A; 602 C; 617 G; 538 T; 2 other;
                                                                                                                                                                                                                                                                                                                    ×
                                                                               Rat connective tissue growth factor encoding DNA.
                                                                                                                                                                                                                                                                                                                    Tamatani T, Tezuka
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 62; Page 161-166; 212pp; Japanese.
                BP.
                                                                                                                                                                                                                                                              98JP-0356183.
97JP-0367699.
              AAX90030 standard; DNA; 2338
                                                                                                                                                                                                                                         98WO-JP05697
                                                                                                                                                                                                                                                                                                 (NISB ) JAPAN TOBACCO INC.
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                         Sakamoto S, Takigawa M,
                                                                                                                                                                                                                                                                                                                                               WPI; 1999-430232/36.
p-PSDB; AAY24379.
                                                                                                                                                                                                                                                                 15-DEC-1998;
25-DEC-1997;
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Best Local Si
Matches 462;
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                                                                 17-SEP-1999
                                                                                                                                                                           Rattus sp.
                                           AAX90030;
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RESULT 13
          AAX90030
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The present sequence encodes a rat connective tissue growth factor (CTGF) polypeptide. The polypeptide may play a significant role in the normal development, growth and repair of mammalian tissue. The polypeptide of control of mammalian tissue. Antisense sequences can be used to inhibit the expression of GTGF and a coll. In particular, the antisense sequences are useful for a mellorating cell proliferative disorders associated with CTGF, of GTGF activity comprises down-regulation. The disorders, which can be of CTGF activity comprises down-regulation. The disorders, which can be treated, are chosen from soleroderma, arthritis, cirribosis, wheatic treated, are chosen from soleroderma, arthritis, cirribosis, adhesions fibrosis, renal fibrosis, atherosclerosis, cardiac fibrosis, adhesions and surgical scarring. The antisense sequences can also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New rat connective tissue growth factor, its related gene and antisense sequences useful for modulating CTGF and treatment of \ensuremath{\mathsf{cell}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat; connective tissue growth factor; CTGF; cell proliferative disorder; connective tissue cell; scleroderma; arthritis; cirrhosis; hepatic fibrosis; renal fibrosis; atherosclerosis; cardiac fibrosis; adhesion; surgical scarring; Ss.
                                                                                       "connective tissue growth factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone 2-4-7 encoding a rat connective tissue growth factor.
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212..1255
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99US-0292036.
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P-PSDB; AAY93340.
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INC.

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AAC77607 to AAC7848 encode the human cancer associated proteins given in AAB4338 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities antidate; prodiferative; vulneary; immunomodulator; antidabetic; antiasthmatic; antithroid; antidabetic; antiasthmatic; antithroid; antidabetic; antipsordective; cardiant; thrombolytic; coagulant; antidamatory; antipsordective; cardiant; thrombolytic; coagulant; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; corportic; vasotropic; antipsoriatic and antiangiogenic. The polyneclectides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Colynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation of fleentiation or mobilisation of immune cells, to treat disorders of haematopoletic cells, autoimmune rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and baccarial or viral infections. The petides, nucleotides, antibodies, agonists and antagonists may be also be used in the exemplification of
                                                                                                                                                                                       Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer
                                                                                                                                                                                                                                         Claim 1; Page 974-975; 2352pp; English
 08-MAR-2000; 2000WO-US05882.
                                                                   (HUMA-) HUMAN GENOME SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the present invention.
                                                                                                   Rosen CA, Ruben SM;
                                                                                                                                     2000-587533/55
                                                                                                                                                     P-PSDB; AAB43830
                                 12-MAR-1999;
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                                                                                   Length 2350;
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                                Sequence 2350 BP; 583 A; 616 C; 610 G; 541 T; 0 other;
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                                                                                Score 427.4; DB 21;
Pred. No. 1.2e-119;
0; Mismatches 51; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detect expression of CTGF in a sample,
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                                                                                  Query Match 83.8%;
Best Local Similarity 90.0%;
Matches 458; Conservative
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                                                                                      0; Gaps
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                                                     21; Length 2553;
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Sequence 2553 BP; 700 A; 569 C; 584 G; 689 T; 11 other;
                                                  58.7%; Score 299.4; DB 2.
99.7%; Pred. No. 7.5e-81;
11ve 0; Mismatches 1.
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Best Local Similarity 99.7*
Matches 300; Conservative
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LENGTH: 2075 base pairs
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-459-717-1
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US-08-880-031-1
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US-09-054-274-1
US-08-459-101A-1
US-08-844-188-45
US-08-86-340-13
US-08-91-03-875-17
US-08-92-635-21
US-08-93-453B-1
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-08-459-041A-1
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Maximum Match 100%
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Sequence
Sequence
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Patent No. 5408040

GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: APALES Spensley Horn Jubas & Lubitz
STREET: Apales
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
                             US-08-764-233A-1
US-08-403-634-3
US-08-913-441B-3
                                                                                                                                                                          US-08-343-428-1
US-08-434-000A-5
                                                                                                                                                                                                                                                                                                                                                                    US-07-862-021B-9
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US-08-435-675B-1
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US-08-750-391-5
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ATTORNEY, AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER: 31.678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435'
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/752,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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NAME/KEY: CDS
                                                                                                               CLONE: DB60R32
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US-08-386-680-1
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Length 2075;
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ZIP: 92037
COMPUTER FEACHE FORM:
COMPUTER FIOPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
COMPUTER: PATON BATO
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,680
FILING DATE: 10-FEB-1995
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/167,628
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Grotendorst, Gary R.
APPLICANT: Grotendorst, Douglas M.,
APPLICANT: Bradham Jr., Douglas M.,
TILLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
WUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
   100.0%; Score 510; DB 1; I
100.0%; Pred. No. 9.8e-139;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Spensley Horn Jubas & Lubitz ADDRESSEE: Spensley Horn Jubas & Lubitz ATSTREET: A225 Executive Square, Suite 1400 CITY: La Jolla STATE: CA
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08386680 Patent No. 5585270 GENERAL INFORMATION:
                      Similarity
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US-08-386-680-1
           Query Match
Best Local Simi.
Matches 510;
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Gaps
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GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                            Query Match 100.0%; Score 510; DB 1; L. Best Local Similarity 100.0%; Pred. No. 9.8e-139; Matches 510; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Spensley Horn Jubas & Lubitz
4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-459-717-1
US-08-459-717-1
Sequence 1, Application US/08459717
; Patent No. 5770209
   31,678
R: PD-1294
REGISTRATION NUMBER: 31,678
REFERENCE,DOCKET NUMBER: PD-1.
TELECOMMUNICATION INFORMATION:
TELEFONE: 619-455-5100
TELEFONE: 619-455-510
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
COLONE: ANGRORY
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121 cgggttaccaatgacaacgcctcctgcaggctagagaagcagagccgcctgtgcatggtc 180
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                                                                                                                                                                                                           APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,302
FILING DATE: 11-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                               E: Spensley Horn Jubas & Lubitz 4225 Executive Square, Suite 1400
                                          1147 TACTACAGGAAGATGTACGGAGACATGGCA 1176
                        481 tactacaggaagatgtacggagacatggca 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/386,680
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US/08/167,628
FILING DATE:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Wetherell, Jr. Ph.D., John W. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                      Sequence 1, Application US/08712302
Patent No: 5783187
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 510; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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US-08-712-302-1
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                                                                                                                                      US-08-712-302-1
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100.0%; Pred. No. 9.8e-139;
tive 0; Mismatches 0; Indels
                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION NOTA:
APPLICATION NUMBER: US/08/459,717
FILING DATE: 02-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                         NAME: Wetherell, Jr. Ph.D., John W. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 9D-1294
TELECOMUNICATION INFORMATION:
TELEPHONE: 619-455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                           FILING DATE: 02-JUN-1995
CLASSIFICATION: 536
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/752,427
FILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100.0
Matches 510; Conservative
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; LOCATION: 130..1177
US-08-459-717-1
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CLONE: DB60R32
La Jolla
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MOLECULE TYPE:
                                                        92037
                                    COUNTRY:
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                                            Length 2075;
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Sequence 1, 6149916
PREENT NO. 16149910N:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bradham Jr.
APPLICANT: Bradham Jr.
APPLICANT: Bradham Jr.
NUMBER OF SEQUENCES: 2
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PRECEDIN Release #1.0, Version #1.25
SOFTWARE: PAPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/097,179
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E. Spensley Horn Jubas & Lubitz
4225 Executive Square, Suite 1400
                                                         100.0%; Score 510; DB 2; 1
100.0%; Pred No. 9.8e-139;
100.0%; Mismatches 0; 1ve
                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,680
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STREET: 422_
CITY: La Jolla
 CDS
130.1177
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                                                                                              Best Local Similarity
Matches 510; Conserv
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, LOCATION:
, US-08-880-031-1
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Best Local Si
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                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: TIBM PC Compatible
COMPUTER: PACENTIN Release #1.0, Version #1.25
SOFTWARE: Pacentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/O8/880,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Grotendorst, Gary R.
APPLICANT: Grotendorst, Douglas M.,
APPLICANT: Breathan T., Douglas M.,
APPLICANT: Breathan T., Douglas M.,
APPLICANT: CONNECTIVE TISSUE GROWTH FACTOR
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEGUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: 4225 Executive Square, Suite 1400
GREET: 4225 Executive Square, Suite 1400
GREET: A 3011a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Wetherell, Jr. Ph.D. John W. REGISTRATION NUMBER: PD-1294
REGISTRENGE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-510
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR PELICATION NUMBER: US/08/167,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08880031
Patent No. 5916756
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 619-45-5-5-1.0 INFORMATION FOR SEC ID NO: 1: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEGUENCE CHARACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
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US-08-880-031-1
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APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
WUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       COMPUTER, TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                    ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
FILING DATE:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Wetherell, Jr. Ph.D., John
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5110
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/080,715
   APPLICANT: Grotendorst, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 619-455-5110 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: 130..1177
US-09-080-715-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: DB60R32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                            ZIP: 92037
                                                                                                                                         CA
                                                                                                                                                             COUNTRY:
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100.0%; Pred. No. 9.8e-139;
iive 0; Mismatches 0;
                                                                                               NAME: Wetherell, Jr. Ph., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 9D-1294
TELECOMMUNICATION INFORMATION:
TELECHONE: 619-455-510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1147 TACTACAGGAAGATGTACGGAGACATGGCA 1176
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                APPLICATION NUMBER: US/08/167,628
                           FILING DATE:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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JS-09-080-715-1
Sequence 1, Application US/09080715
Setent No. 6190884
SENERAL INFORMATION:
10-FEB-1995
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Matches 510; Conservative
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                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDN
IMMEDIATE SOURCE:
CLONE: DB60R32
FEATURE:
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; LOCATION: 130
US-09-097-179-1
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                                                                                                                            667 GCGGCTTACCGACTGGAAGACACGTTTGGCCCAGACCCAACTATGATTAGAGCCAACTGC 726
                                                                                    1 gegettacegactggaagacacgtttggcccagacccaactatgattagagccaactgc 60
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    ; Score 510; DB 4; Length 2075; Pred. No. 9.8e-139; 0; Mismatches 0; Indels 0
    100.0%;
Query Match
Best Local Similarity 100.(
Matches 510; Conservative
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GENERAL INFURMATION: of South Florida
APPLICANT: GIOLEMGOST, GATY
APPLICANT: GIOLEMGOST, GATY
APPLICANT: GIOLEMGOST, GATY
TITLE OF INFURITON: CONNECTIVE TISSUE GROWTH FACTOR
TITLE OF INFURITON: CONNECTIVE TISSUE
GURRENT APPLICATION NUMBER: US/09/054,368
CURRENT APPLICATION NUMBER: 08/386,680
EARLIER APPLICATION NUMBER: 08/386,680
EARLIER APPLICATION NUMBER: 08/459,717
EARLIER APPLICATION NUMBER: 08/459,717
EARLIER PILING DATE: 1995-06-02
EARLIER TILING DATE: 1993-12-14
EARLIER FILING DATE: 1993-12-14
SARLIER FILING DATE: 1993-12-14
SUMBER OF SEQ ID NOS: 9 NUMBER: 8 SECON NOWER: 9 SECO
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Sequence 1, Application US/09054368
Sequence 1, 6069006
Patent No. 6069006
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Matches 510; Conservative
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LOCATION: (1025)...(2074)
US-09-054-368-1
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Sequence 1. Application PC/TUS9608140
Sequence 1. Application PC/TUS9608140
Sequence 1. Information: University of South Florida Applicant: University of South Florida Applicant: University of South Florida Applicant Connector Connector Connector Connector Connector Connector Florida Application P.C.
CORRESPONDENCE FLORIDA RICHARDSON P.C.
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: AJ25 Executive Square, Suite 1400
STREET: AJ01la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Floppy disk
COMPUTER: TBM PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, version #1.25
SOFTWARE: PATENTIN DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08140
APPLICATION NUMBER: PCT/US96
CLASSIFICATION:
ATTENNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 510; DB 5; L 100.0%; Pred. No. 9.8e-139; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
ANDE: Halle, ph.D., Lisa A.
NAME: Halle, ph.D., Lisa A.
REGISTRATION NUMBER: 30,347
REFERENCE/DOKEY 100,144/003W01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 1:
INFORMATION FOR SEQ ID NO: 1:
LENGTH: 2075 base pairs
                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 130..1177
pcr-us96-08140-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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IMMENTAR
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Best Local Similarity
Matches 510; Conservê
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CLONE: CTGF
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1742 aggocttgcgaagctgacctggaagagaacattaagaagggcaaaaagtgcatccgtact 1801
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                                                                                                                                                                                                                                                                           421 atcaagacctgtgcctgccattacaactgtcccggagacaatgacatctttgaatcgctg
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APPLICANT: Grotendorst, Gary R.
TITLE OF INVENTION: WETHODS OF DIAGNOSING A PATHOLOGY
TITLE OF INVENTION: CHARACTERIZED BY A CELL PROLIFERATIVE
TITLE OF INVENTION: DISORDER ASSOCIATED WITH CONNECTIVE
TITLE OF INVENTION: TISSUE GROWTH FACTOR (Amended)
FILE REFERRANCE: 07414/003002
CURRENT FILLING DATE: 1998-033-03
CURRENT FILLING DATE: 1995-02-10
EARLIER APPLICATION NUMBER: 08/459,717
EARLIER FILLING DATE: 1995-06-02
EARLIER APPLICATION NUMBER: 08/459,717
EARLIER FILLING DATE: 1995-06-02
EARLIER FILLING DATE: 1995-06-02
EARLIER FILLING DATE: 1993-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 510; DB 4; L; Pred. No. 1.1e-138; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                           FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09056704
Patent No. 6232064
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100.0%;
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Best Local Similarity 100.
Matches 510; Conservative
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; LOCATION: (1025)...(2074)
US-09-056-704-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NOS:
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SEQ ID NO 1
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   aggccttgcgaagctgacctggaagagaacattaagaagggcaaaaagtgcatccgtact
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APPLICANT: University of South Florida
APPLICANT: Bradham, Jr., Douglass M.
APPLICANT: Bradham, Jr., Douglass M.
TITLE OF INVENTION: METHODS OF IDENTIFYING A COMPOSITION
TITLE OF INVENTION: PACTOR EXPRESSION (Amended)
TITLE OF INVENTION: FACTOR EXPRESSION (Amended)
TITLE OF INVENTION: PACTOR EXPRESSION (Amended)
TITLE OF INVENTION: PACTOR EXPRESSION (Amended)
CURRENT APPLICATION NUMBER: US/09/054,274
CURRENT FILING DATE: 1998-04-02
EARLIER FILING DATE: 1998-02-10
EARLIER FILING DATE: 1995-02-10
EARLIER FILING DATE: 1995-02-10
EARLIER FILING DATE: 1995-02-10
EARLIER FILING DATE: 1995-02-10
EARLIER FILING DATE: 1995-12-14
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100.0%; Pred. No. 1.1e-138;
iive 0; Mismatches 0;
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Patent No. 6150101
GENERAL INFORMATION:
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; LOCATION: (1025)...(2074)
US-09-054-274-1
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Sequence 1, Application US/08459101A
Sequence 1, Application
GENERAL INFORMATION:
APPLICANT: L1, ET AL.
APPLICANT: L1, ET AL.
APPLICANT: Connective Tissue Growth Factor-2
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART 6 OLSTEIN STREET: 6 BECKER FARM ROAD CITY: ROSELAND STATE: NEW JERSEY COUNTRY: USA ZIP: 07068
COMPUTER READBLE FORM: MEDIUM TYPE: 3.5 INCH DISKETTE MEDIUM TYPE: 3.5 INCH DISKETTE COMPUTER: IBM PS/2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUFTWARE: MORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,101A
FILING DATE: June 2, 1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                               325800-317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US94/07736 FILING DATE: 12 JUL 94 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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APPLICATION NUMBER:
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US-08-459-101A-1
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355 accaccacctgccggtggagttcaagtgcctgacggcgaggtcatgaagaagaacatg 414
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                                                                  685 AAATGTATTGTTGAAAAAAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATC 744
                                       aactgoctggtccagaccacagagtggagcgctgttccaagacctgtgggatgggcatc 114
                                                                                                                                                                175 atggtcaggccttgcgaagctgacctggaagagacattaagaaggcaaaaagtgcatc
                                                                                                                                                                                                                          235 cgtactcccaaaatctccaagcctatcaagtttgagctttctggctgcaccagcatgaag
                                                                                                                  pred. No. 1.3e-35;
0; Mismatches 160; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/844,188 FILING DATE: CLASSTORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Routh, Mark
APPLICANT: Follard, Michael R.
APPLICANT: Gardineau, Guy
APPLICANT: Schwab, George E.
TITLE OF INVENTION: Pesticidal Toxins
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
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US-08-844-188-45
US-08-844-188-45
; Sequence 45, Application US/08844188
; Sequence 6127180
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TELEPHONE: 352-375-8100
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NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,3
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FILING DATE: 19-APR-1996
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
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PRIOR APPLICATION DATA:
      Best Local Similarity 61.0
Matches 250; Conservative
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STATE: FT.
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Score 34.2; DB 3; Length 293; Pred. No. 0.42; 0; Mismatches 38; Indels

6.7%;

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Query Match 6.7%
Best Local Similarity 60.0%
Matches 57; Conservative
    US-08-866-340-13
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Patent No. 6020318
GENERAL INFORMATION:
APPLICANT: B194y, Pascal
APPLICANT: B194y, Pascal
APPLICANT: Ramchandan1 , Shyam
TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC
TITLE OF INVENTION: SEQUENCES AND ANTISENSE OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                 Score 36; DB 3; Length 1158;
Pred. No. 0.21;
0; Mismatches 110; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/08/866,340
FILING DATE:
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NAME: KEOWN, WAYNE A.
REGISTRATION NUMBER: 33,923
REFERENCE/DOCKET NUMBER: 106.3
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HALE AND DORR LLP
                                                                                                            ; MOLECULE TYPE: DNA (genomic)
US-08-844-188-45
                                                                                                                                                                                                   Query Match 7.1%;
Best Local Similarity 48.1%;
Matches 102; Conservative
SEQUENCE CHARACTERISTICS:
LENGTH: 1158 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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LENGTH: 293 base pairs
TYPE: nucleic acid
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STATE: MA
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US-08-866-340-13/c
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APPLICANT: Bigey, Pascal
APPLICANT: Bigey, Pascal
APPLICANT: Ramchandani, Shyam
TITLE OF INVENTION: DNA METHYLFRANSFERASE GENOMIC SEQUENCES AND ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES
123 ggttaccaatgacaacgcctcctgcaggctagaagcagagccgcctgtgcatggtcag 182
                                   249 GGTTCCCAGTCACATGGCCTTCTGCAAGCCTGCTGAGAATTCCCACCAGAGCCCCGTCAG 190
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Pred. No. 0.42;
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                                                                                                           183 gccttgcgaagctgacctggaagaagaacattaaga 217
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CURRENT APPLICATION NUMBER: US/09/103,875A
CURRENT FILING DATE: 1998-06-24
EARLIER APPLICATION NUMBER: 60/069,865
EARLIER FILING DATE: 1997-12-17
EARLIER FILING DATE: 1997-12-17
EARLIER FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 138
SEQ ID NO 17
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Matches 57; Conservative
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ORGANISM: Homo sapiens
US-09-103-875-17
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em_estro18:'
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em_estin3:'
em_estin4:'
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em_estro2:
em_estro3:
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em_estpl6:
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4109.131 Million cell updates/sec
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1 gcggcttaccgactggaaga.....agatgtacggagacatggca 510
                                                                                                                                                                                August 20, 2001, 21:23:54 ; Search time 1173.23 Seconds
                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10228115 segs, 4726426750 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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em_esthum8:
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em_esthum1:
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9b_est13:
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9b_est15:
9b_est16:
9b_est17:
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gb_est23:*
gb_est24:*
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gb_est34:*
gb_est35:*
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gb_est20:
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gb_est2:*
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| 1913 | 90-set1|11.\*\*
| 1914 | 90-set1|11.\*\*
| 1915 | 90-set1|11.\*\*
| 1916 | 90-set1|11.\*\*
| 1917 | 90-set1|11.\*\*
| 1918 | 90-set1|11.\*\*
| 1919 | 90-set1|11.\*\*
| 1910 | 90-set1|11.\*\*

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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// Organism="Homo sapiens"
// Organism="Homo sapiens"
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// Clone="InAGE: 401335"
// Clone="InAGE: 401335"
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// Lab_host="DH10B (phage-resistant)"
// Note="Organ: small intestine; Vector: pcWv-SPORT6;
// Site_1: Not!; Site_2: Sall; Cloned unidirectionally;
// Oliqo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM10108 row: b column: 24
High quality sequence start: 2
High quality sequence stop: 678.
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                                                                 HIT human cDNA project

HIT human cDNA project

Unpublished (2000)

Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

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Tell: 81-438-52-3952

Email: genomics@thi.co.jp

Fax: 81-438-52-3952

Email: genomics@thi.co.jp

Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                0;
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 854) Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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Best Local Similarity 97.1%; Pred. No. 9.2e-125;
Matches 470; Conservative 0; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                      /tissue_type="whole embryo, mainly head"
/tissue_type="wholyo, 10 weeks"
/note="vector: pME18SFL3"
/note="vector: pME18SFL3"
/note="vector: pME18SFL3"
                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEMBA1003198"
/clone_lib="HEMBA1"
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                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I toases; 1 to 6789
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infoelmage.llnl.gov) for further information. Seg primer: -40RP from Gibco.
High quality sequence stop: 471.
         61 ctggtccagaccacagagtggagcgcctgttccaagacctgtgggatgggcatctccacc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cgggttaccaatgacaacgcctcctgcaggctagagaagcagagccgcctgtgcatggtc 180
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Pred. No. 5.4e-116;
0; Mismatches 48; Indels
                                                          /organism-"Mus musculus"
/strain-"C3H x 101 (F1 stock)"
/db_xref="taxon:10090"
/clone-"IMAGE:2780107"
/clone_lib-"Soares_mouse_NMIE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="newborn"
/lab_host="DH10B"
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1. .678
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Best Local Similarity 90.6%;
Matches 461; Conservative
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zp70a06.rl Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625522 5' similar to gb:M92934 CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (HUMAN);, mRNA sequence.
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
Walte,Y., Wylie,T., Waterston,R. and Wilson,R.
WashGround Human EST Project
Conpublished (1997)
Contact: Wilson RK
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/clone="IMAGE:62552"
/clone="IMAGE:62552"
/clone="taxon:966"
/clone="taxon:966"
/dev_stage="umbilical vein, 1 passage"
/lab_host="sour (kanamycin resistant)"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
Xhol; Cloned unidirectionally, Primer: Oligo dT.
Umbilical vein endothelial cells, passaged once. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATICGGCACGAG 3' -3' adaptor sequence: 5'
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: est@watson.wustl.edu
361 accetgeceggtggagttcaagtgecetgaeggegaggtcatgaagaagaacatgatgtte 420
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/db_xref="GDB:5047676"
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AA187390.1 GI:1773616
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="LTI_NFLO06_PL2"
/tissue_type="placenta"
/note="vector: pcMvSPORT 6; Site_1: Not!; 1st strand cDNA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 879)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Li,W.B., Gruber,C., Jessee,J. and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Bp 191 91006 EVRY cedex - France

Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
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9
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Homo sapiens cDNA clone CSODI011XE17
                                                                      6; Gaps
                                   Length 487;
others
                                                       Indels
                                 Score 410.4; DB 3;
Pred. No. 1.2e-109;
0; Mismatches 5;
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AL547439 LTI_NFL006_PL2
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AL547439
AL547439.1 GI:12881511
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Mus musculus
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Eukaryota; Metazoa; Rodentia; Sciurognathl; Muridae; Murinae; Mus.
Mamalia; Eutheria; Rodentia; Sciurognathl; Muridae; Murinae; Mus.
1 (bases 1 to 696)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Marra,M., Hillier,L., Lecy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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mRNA EST 12-FEB-139/
3NME12 5 Mus musculus cDNA clone
to gb:M70641 Mouse FISP-12 protein (MOUSE
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                                                                                                                                                                                           Score 410; DB 106;
Pred. No. 1.9e-109;
2: Mismatches 2;
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WashU-HHMI Mouse EST Project
                                                                                                                                                                                         Query Match 80.4%; Score 410; DB Best Local Similarity 98.8%; Pred. No. 1.9e Matches 421; Conservative 2; Mismatches
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
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AA221075.1 GI:1840244
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494 GTACGGAGACATGGC 508
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                                                                                                                                                                                                                                                                                                                                                                       31, on total mouse RNA [provided by Minoru Ko, Wayne State Univ.]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

174 c 169 g 152 t l others
                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:406718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 AGAGT-GAGGGCCTGTTCTAAGACCTGTGGGGATTGCGACTTCCCACCCGAGTTACCAATGA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 CGGGGTGTGCACAGACGCCGCTGCACACCGCACAGAACCACCACTCTGCCAGTGGA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caacgcctcctgcaggctagagaagcagagccgcctgtgcatggtcaggccttgcgaagc 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 TGACCTGGAGGAAAACATTAAGAAGGGCAAAAAGTGCATCCGGACACCTAAAATCGCCAA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375 gttcaagtgccctgacggcgaggtcatgaagaagaacatgatgttcatcaagacctgtgc 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 ggaagacacgtttggcccagacccaactatgattagagccaactgcctggtccagaccac 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 tggagtatgtaccgacggccgatgctgcacccccacagaaccaccacctgccggtgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 gcctatcaagtttgagctttctggctgcaccagcatgaagacataccgagctaaattctg
                Forest Park Parkway, Box 8501, St. Louis, MO 63108
314 286 1801
314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.3%; Score 409.4; DB 4; Length 696; 90.5%; Pred. No. 2.6e-109; Live 0; Mismatches 46; Indels 1.
                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:660870"
/clone_lib="Soares mouse 3NME12 5"
Washington University School of MedicineP
A44 Forest Park Parkway, Box 8501, St. Lv
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                   /tissue_type="fetus"
/dev_stage="12.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                       Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 499.
Location/Qualifiers
1. .696
                                                                                                                                                                                                             /organism-"Mus musculus"
                                                                                                                                                                                                                              /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                      /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 436)
1 (bases 1 to 436)
2 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wal, C., Clayton, R.A.,
Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald

L.M., Fitzhugh, M.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,
Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Fenzie, A., Fischer, C., Hastings, G.A., He, W.W.
HU, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
Kunsch, C., Hung, J., Xu, C., Yu, G.L.,
Wei, Y.F., Wing, J., Xu, C., Yu, G.L.,
Wei, Y.F., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: MI3 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ctggtccagaccacagagtggagcgcctgttccaagacctgtggggatgggcatctccacc 120
21-APR-1997
end similar to
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AA373233 436 bp mRNA EST
EST85240 HSC172 cells I Homo sapiens cDNA 5' er
connective tissue growth factor, mRNA sequence.
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llarity 97.9%; Pred. No. 3.4e-107;
Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research 9712 Medical Center Drive, Rockville, Tel: 3018699056
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                                                                                                                      AA373233.1 GI:2025553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Other_ESTs: THC166347
Contact: Kerlavage, AR
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Matches 427; Conserv
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Tel: +55-11-2704922
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/clone_lib="Soares melanocyte"
/tissue_type="melanocyte"
/tissue_type="melanocyte"
/tishost="0H10B (ampicillin resistant)"
/note="Vector: pr7T3D (Pharmacia) with a modified
/note="Vector: pr7T3D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 57)

Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman

##, Hullman, M., Kucaba, T., Le, M., Lenon, G., Marra, M., Parsons, J., Rikhn, L., Rohhfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                               N3234 577 bp mRNA EST 10-JAN-1996 y 722a09.rl Soares melanocyte 2NbHM Homo sapiens cDNA clone y 1485.267256 5' similar to 9b:M92934 CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (HUMAN);, mRNA sequence.
                                 240
                                                                                         /organism="Homo sapiens"
/db_xref="GDB:3876898"
/db_xref="taxon:9606"
/clone="TMAGE:267256"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 340.
Location/Qualifiers
1. 577
                                                                                                                                                                                                                                                                                                                                                                                                    N32344.1 GI:1152743
                                                                                                                                                                                                                                                                              421 CATCAAGACCTGTGCC 436
                                                                                                                                                                                                                                                                  catcaagacctgtgcc 435
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AUTHORS
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VERSION
KEYWORDS
SOURCE
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Homo sapiens

Homo sapiens

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;

Bukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.

I (bases 1 to 595)

I (bases 1 to 595)

Nagai, M.A., da sliva, W. Jr., Zago, M.A., Bordin, S., Costa, F. F., Coldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Burstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O Har, M.J., Soares, F., Brentanl, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BEB16120 595 bp mRNA EST 21-SEP-2000 RC5-BN0193-140600-032-B01 BN0193 Homo sapiens CDNA, mRNA sequence. BEB16120 GI:10248354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed sequence tags proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                               Length 577;
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                                                                                                                                                               Score 394; DB 159;
Pred. No. 8.3e-105;
0; Mismatches 1;
                                                                                                                                                                     Query Match 77.3%;
Best Local Similarity 99.3%;
Matches 416; Conservative
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Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
                                                                                                                                                                                                  Brazil
Tel: +55-11-2704922
                                                                                                                                                                                                                                     Fax: +55-11-2707001
                                          Simpson, A.J.
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                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0193"
/dev_stage="Adult"
/note="Organ: breast_normal; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
77 a 147 c 135 g 136 t
Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC5-BN0193-140
600-032-B01&t3=2000-06-14&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 3
High quality sequence start: 3
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammala; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 415)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HT0489 Homo sapiens cDNA, mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 caacgcctcctgcaggctagagaagcagagcctgtgcatggtcaggccttgcgaagc 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 tggagtatgtaccgacggccgatgctgcacccccacagaaccaccacctgccggtgga 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 gitcaagigcccigacggcgaggicatgaagaagaacaigaigitcaicaagaccigigc 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CAACGCCTCCTGCAGGCTAGAGAAGCAGAGCCGCCTGTGCATGGTCAGGCCTTGCGATGT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 TGGAGTATGTACCGACGCCGCTGCTGCACCCCCCACAGAACCACCACCTGCCGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 GTTCAAGTGCCCTGACGCGAGGTCATGAAGAACATGATCATCATCAAGACCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 gectateaagtttgagetttetggetgeaceageatgaagaeataeegagetaaattetg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 tgacctggaagagaacattaagaagggcaaaagtgcatccgtactcccaaaatctccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 363.2; DB 140; Length 595;
Pred. No. 9e-96;
0; Mismatches 8; Indels 0;
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MR3-HT0489-250200-103-a05 HT
BE166172.1 GI:8628893
                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 71.2%;
Local Similarity 97.9%;
Nes 368; Conservative (
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                               Source
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ACCESSION
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BE166172/C
                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
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AUTHORS
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1. .415
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Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR3.HT0489-250
200-103-a05&t3=2000-02-25&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 415.
Location/Qualifiers
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Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                        Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 cgggttaccaatgacaacgcctcctgcaggctagagaagcagagccgcctgtgcatggtc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366 GCGGCTTACCGACTGGAAGACACGTTTGGCCCAGACCCAACTATGATTAGAGCCAACTGC 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ctggtccagaccacagagtggagcgcctgttccaagacctgtgggatgggcatctccacc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 aggoottgcgaagctgacctggaagagaacattaagaagggcaaaaagtgcatccgtact
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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Best Local Similarity 97.3%; Pred. No. 2.3e-91
Matches 354; Conservative 0; Mismatches 1
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1...491
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/note="forgan: breast normal; Vector: puc18; Site_l: Smal;
/note="forgan: breast normal; Amin1-library was made by cloning products
slite_listing normal; Amin1-library normal; No. 196,716 - Ludwig Institute for Cancer Research)
No. 196,716 - Ludwig Institute for Cancer Research
No. 196,
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-RC5-BN0193-120
(0.055-A03&t3-2000-09-12&t4-1)
Seq primer: puc 18 forward
High quality sequence stert: 128
High quality sequence stert: 128
High quality sequence step: 488.
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Homo 
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RC5-BN0193-120900-035-A03 BN0193 Homo sapiens CDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                           DB 144; Length 491;
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20202663
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Pred. No. 7.2e-91;
0; Mismatches 12;
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Best Local Similarity 96.6%;
Matches 364; Conservative (
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COMMENT
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SOURCE
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BF082233
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/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
/note="Organ: brinity A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
No. 196,716 - Ludwig Institute for Cancer Research)
No. 196,716 - Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was derived from the FAPESP/LICR Human Cancer Genome This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2-wRO-BNO115-210 8800-006-903&t3-2000-08-21Et4-1) Seq primer: puc 18 forward High quality sequence start: 44 High quality sequence start: 44 High quality sequence stop: 631.
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                                                                                               BE926068 631 bp mRNA EST 02-OCT-2000
MRO-BN0115-210800-006-903 BN0115 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryott, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 631)
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                          02-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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pred. No. 3.9e-91;
0; Mismatches 1;
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Re
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BE926068.1 GI:10452144
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hes 359; Conservative
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BF162951 800 bp mRNA EST 30-OCT-2000
G01767349F1 NCT_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3983125 5',
mRNA sequence.
BF162951
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 800)
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/lab_host="DH10B" vector: pCMV-SPORT6; Site_1: Sal1:
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                 121 TCCAAGCCTATCAAGTTTGAGCTTTCTGGCTGCACCAGCATGAAGACATACCGAGCTAAA 180
                                                                                                                                                                                                                                                                                                                                           370 gtggagttcaagtgccctgacggcgaggtcatgaagaagaacatgatgttcatcaagacc 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tgtgcctgccattacaactgtcccggagacaatgacatctttgaatcgctgtactacagg 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIF-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
Unpublished (1999)
                                                                                          130 aatgacaacgcctcctgcaggctagagaagcagagcgcctgtgcatggtcaggccttgc
                                                                                                             tecaageetateaagtttgagetttetggetgeaceageatgaagaeataeegagetaaa
                                                                                                                                                                                                                                                                                                                    ttctgtggagtatgtaccgacggccgatgctgcacccccacagaaccaccacctgccg
                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Emall: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                     Length 388;
                                                         Indels
                   Score 340; DB 136;
Pred. No. 5.1e-89;
0; Mismatches 25;
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Plate: LLAM9183 row: a column: 14
High quality sequence stop: 683.
Location/Qualifiers
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/strain="CZECH II (feral)"
/db_xref="taxon:10090"
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/clone_lib="NCI_CGAP_Lu29"
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Sonstegard, T.S., Capuco, A.V., Van Tassell, C.P., Ashwell, M.S. and Wells, K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
Unpublished (2000)
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore
                                  254 agcctatcaagtttgagctttctggctgcaccagcatgaagacataccgagctaaattct 313
   83
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25 ACAACGCCTCCTGCAGGCTAGAGAAGCAGAGCCGGCTGT-CACCTGCAGGCCTAGCGACG
                                                                                                                           144 AGCCTATCAAGTTTGAGCTTTCTGGCTGCACCAGCATGAAGGCATACCGAGCTAAATTCT
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163702 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
BE479129
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Balg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
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/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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Seq primer: ATTTAGGTGACACTATAG
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187 a 219 c 233 g 161 t
                                                              6; Gaps
                           Query Match 66.5%; Score 339.4; DB 145; Length 800; Best Local Similarity 84.0%; Pred. No. 9.3e-89; Matches 431; Conservative 0; Mismatches 76; Indels 6;
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N-PSDB; AAA11281.
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14-DEC-1998;
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                                                                                            August 20, 2001, 22:04:44 ; Search time 61.48 Seconds
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36 404 42.6 354 20 AAY34190 Human connect 37 404 42.6 354 20 AAY34190 Human connect 33 4 42.6 354 21 AAY81438 Human Wisp-3 39 400.5 42.2 335 21 AAY59247 Human Wisp-1 400.5 42.2 345 20 AAY17642 Human Connect 41 400.5 42.2 345 20 AAY17640 Human Wisp-1 42 400.5 42.2 345 20 AAY17640 Human Wisp-1 43 400.5 42.2 367 20 AAY17643 Human Wisp-1 44 400.5 42.2 367 20 AAY17643 Human Wisp-1 45 400.5 42.2 367 20 AAY17643 Human Wisp-1 45 400.5 42.2 367 20 AAY17643 Human Wisp-1 45 400.5 42.2 367 20 AAY17641 Human Wisp-1 AAY92941 standard; Protein; 172 AA.  AAY92941;  OB-NOV-2000 (first entry)  Human connective tissue growth factor protein fragment.  Human connective tissue growth factor; CTGF; mitogen; antibody; liv fibroproliferative disease; scleroderma; fidrosathy; architcils hypertropic scarring; atherosclerosis; diabetic nephropathy: retinon	32	404	2	339	20	AAY17656	
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		an; con	nective	tissue	gro	wth factor; CTGF; mit	antibody; liver
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Query Match
Best Local Similarity 100.0
Matches 170; Conservative
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N-PSDB; AAT04226.
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AAR79964
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                                                          This sequence represents a fragment of the human connective tissue growth factor (CTGE) Polypeptide which has mitogenic activity. The growth factor (CTGE) Polypeptide which has mitogenic activity. The sequence covers the amino acids encoded by exons 4 and 5 of the full sequence covers the amino acids encoded by exons 4 and 5 of the full length cDNA sequence (AAA11280). The protein can be used to raise antibodies which specifically bind to CTGE and are used to rise antibodies which specifically bind to CTGE and are used to treat a antibodies which associated dispass of disorder, e.g. a fibroproliferative fibrosis, such as kidney fibrosis, scheroderm, pulmonary fibrosis, liver fibrosis, arthritis, hypertropic scarring, atherosclerosis, diabetic nephropathy and retinopathy, hypertension, kidney disorders, and cardiovascular disorders. The protein is also useful in wound healing, bone and tissue repair.
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                      1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
                                                                                                                                                                                                                                                                                 Connective tissue growth factor; CTGF; bone; cartilage; vulnerary; wound healing; osteoporosis; osteoarthritis; osteochondrytis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Connective Tissue Growth Factor composition - for inducing bone, tissue and cartilage formation and wound healing
  New fragment of connective tissue growth factor (CTGF) polypeptide having mitogenic activity, useful in wound healing, bone and tissue
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                                                 Disclosure; Fig 3; 71pp; English.
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Best Local Similarity 100.
Matches 170; Conservative
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N-PSDB; AAT59618.
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repair
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Recombinant CTGF can be produced in prokaryotic or eukaryotic host secombinant CTGF can be produced in prokaryotic or eukaryotic host cells utilising an isolated CTGF gene (AAT59618). Compsis.

cells utilising an isolated CTGF gene (AAT59618). Compsis.

induce bonding formation, e.g. to treat osteopporesis, induce bonding formation, e.g. to treat osteopporesis, contacton, and to induce wound healing. It can also be used in formation, and to induce wound healing. It can also be used in culture systems e.g. to expand stem cells or chondrocytes prior to re-implantation. CTGF is more stable to protease degradation than other growth factors used as prior art wound healing agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New connective tissue growth factor - used to develop prods. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Connective tissue growth factor; CTGF; wound healing; vulnerary; cell proliferation; cancer; fibrosis; atherosclerosis; diagnosis
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100.0%; Pred. No. 9.1e-86;
.ive 0; Mismatches 0;
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93US-0167628.
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N-PSDB; AAT45360;
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                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                           Query Match
              N-PSDB;
                                                                 nealing
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                                                                                                                                                                                                                                                                                                            240 rpceadleenikkgkkcirtpkiskpikfelsgctsmktyrakfcgvctdgrcctphrtt 299
                                                                                                                                                                                                                                                                                                                                                61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                              1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
                                                          Novel human connective tissue growth factor (CTGF) (AAR79964) is related immunologically and biologically to platelet-derived growth factor (PDGF), but is the product of a distinct gene.

GTGF is mitogenic and ano fibroblastic capat for cells. It is produced by endothelial and fibroblastic cells, and probably acts as a growth factor in wound healing. Recombinant CTGF can be obtd. by expression of CDNA clone DBG0R32 (AAT04226) in transformed host cells. It is used to accelerate wound healing, and to raise antibodies useful in detecting disorders associated with overgrowth of cells, such as cancer, fibrotic diseases and atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Connective tissue growth factor; CTGF; mitogen; cell proliferation; wound healing; cancer; tumour; fibrosis; glaucoma; atherosclerosis; scleroderma; arthritis, cirrhosis; scar; diagnosis; therapy.
wound healing and for diagnosis and therapy of cell proliferative
                                                                                                                                                                                                                                                                      .,
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                                                                                                                                                                                                                                          Query Match 100.0%; Score 948; DB 16; Length 349; Best Local Similarity 100.0%; Pred. No. 9.2e-86; Matches 170; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                   121 TLPVEFKCPDGEVWKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 170
                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Glycosylation
/note= "potential N-glycosylation site"
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/note= "potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human connective tissue growth factor.
                                    Claim 1; Column 19-20; 12pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW09089 standard; Protein; 349 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo saplens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-1996;
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              disorders
                                                                                                                                                                                                          Sequence
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Connective tissue growth factor; CTGF; human; connective tissue cell; proliferative disease; platelet-derived growth factor; PDGF; development; tissue growth; repair; umbilical vein endothelial cell; HUVE cell; antibody; wound healing; cancer; fibrotic disease; atherosclerosis; inhibitor; protease degradation; growth factor; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
                                                                                                                                                                Novel human connective tissue growth factor (CTGF) (AAW09089) is a PDGF-immunorelated protein that may play a significant role in the normal development, growth and repair of human tissue and probably functions as a growth factor in wound healing. CTGF may be involved in diseases in which there is an overgrowth of connective tissue cells, such as cancer, tumour formation and growth, fibrotic diseases (e.g. pulmonary fibrosis, kidney fibrosis, glaucoma) and atherosclerosis. Recombinant CTGF can be produced in transformed host cells utilising a cDWA clone isolated from a HUVEC library. It can be used to accelerate wound healing. CTGF inhibitors can be used to treat atherosclerosis and fibrotic diseases such as scleroderma, arthritis, liver cirrhosis, and scarring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
                                          Connective tissue growth factor coding sequence and protein - used in the treatment of proliferative disorders and to accelerate wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 948; DB 18;
Pred. No. 9.2e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                          Claim 19; Page 50-52; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW11302 standard; Protein; 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Connective tissue growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.08;
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93US-0167628.
95US-0386680.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100. Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          349 AA;
AAT58534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-AUG-1991;
14-DEC-1993;
10-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-AUG-1991;
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Human connective tissue growth factor
                                      Claim 9; Column 15-18; 11pp; English.
                                                                                                                                                                                                                                                      AAW62084 standard; Protein; 349
                                                                                                                                                                                                                                                                                                                                                         91US-0752427.
93US-0167628.
96US-0712302.
                                                                                                                                                                                                                                                                                                                                                96US-0712302
                                                                                                                                 due to the high Cys content.
                                                                                                                                                               Best_Local Similarity
Matches 170; Conserv
     WPI; 1997-051180/05.
                                                                                                                                                                                                                                                                                                          atherosclerosis;
                                                                                                                                            349 AA;
           N-PSDB; AAT51234
                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                  11-SEP-1996;
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11-SEP-1996;
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                                                                                                                                                                                                                                                                  AAW62084;
                                                                                                                                             Sequence
                                                                                                                                                            Query Match
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A method has been developed for ameliorating a cell proliferative disorder associated with connective tissue growth factor (CTGF). The disorder associated with connective tissue growth factor (CTGF). The binds to CTGF and not to platelet-derived growth factor (PDGF), to the bits of the disorder. CTGF is related immunologically and biologically site of the disorder. GTGF is related immunologically and biologically to PDGF. The present sequence represents CTGF. The method is used to treat conditions involving the overgrowth of connective tissue cells such as cancer, atherosclerosis and other fibrotic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
                                                                                                                                                         Ameliorating cell proliferative disorder associated with connective tissue growth factor - comprises the administration of an antibody which binds to connective tissue growth factor and not to platelet-derived growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGF; connective tissue growth factor; human; fibrotic disease; cell proliferative disorder; atherosclerosis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 948; DB 19;
100.0%; Pred. No. 9.2e-86;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                         Example 6; Column 17-20; 11pp; English.
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95US-0386680.
96US-0712302.
97US-0880031.
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                                                          Grotendorst GR;
     (UYSF-) UNIV SOUTH FLORIDA.
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Best Local Similarity 100.
Matches 170; Conservative
                                                                                                           WPI; 1998-426958/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 AA;
                                                                                                                                  N-PSDB; AAV38085
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11-SEP-1996;
20-JUN-1997;
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                                                             Bradham DM,
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δλ
                                                                                                                                                                                                                                This sequence represents the human connective tissue growth factor (CTGF): CTGF is related immunologically and biologically to cape of careford growth factor (PDGF), but is encoded by an unrelated platelet-derived growth factor (PDGF), but is encoded by an unrelated cape of evelopment, growth, and repair of human tissue, similarly to PDGF. The development, growth, and repair of human tissue, similarly to PDGF. The CDMA encoding this sequence was isolated by screening a CDNA library from CDMA encoding this sequence was isolated by screening a CDNA library from CDMA encoding this sequence would healing. Also, elevated levels of CTGF may be diagnostic of proliferative diseases involving outgrowth of CTGF may be diagnostic of proliferative diseases and enterosclerosis. All of these diseases can be treated with reagents cactive with CTGF, such as antibodies (which can also serve as assay reactive with CTGF such as antibodies (which can also serve as assay captable, and less susceptible to protease degradation than PDGF, and conter growth factors involved in wound healing. This is believed to be content of the content o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; connective tissue growth factor; CTGF; PDGF; diagnosis; cancer; platelet derived growth factor; ameliorating cell proliferative disorder; atherosclerosis; fibrotic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                              New nucleic acid encoding connective tissue growth factor - useful for accelerating wound healing, also for diagnosis and treatment of proliferative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAYRLEDJFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV
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ilarity 100.0%; Pred. No. 9.2e-86;
Conservative 0; Mismatches 0;
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Grotendorst GR;

Bradham DM,

SOUTH FLORIDA.

(UYSF-) UNIV

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Indels

Length 349;

9 Gaps

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14-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY92939;
                                                                                                                                                                                                                         Seguence
                                                          Use of
                                                                                                                                                                                                                                                                                                                              61
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                                                                                 This sequence is the human connective tissue growth factor (CTGF). The invention relates to a method of detecting a cell proliferative disorder comprising comparing the level of CTGF in a sample against a control, where an increase is indicative of a cell proliferative disorder (fibrotic disease or atherosclerosis). The method is used to detect cell proliferative disorders such as fibrotic disease and atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGF; connective tissue growth factor; bone formation; tissue; arthritis; wound healing; cartilage formation; osteoporosis; osteoarthritis; burn; osteochondrytis; skeletal disorder; hypertrophic scar; protease; pDGF; degradation; vascular hypertrophy; platelet derived growth factor.
                                                                                                                                                                                                                                                                      61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
                                                                                                                                                                                                    Gaps
                                     Detecting cell proliferative disorders such as fibrotic disease and
                                                                                                                                                                                                                      1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV
                                                                                                                                                                                                    ö
                                                                                                                                                                               100.0%; Score 948; DB 20; Length 349; 100.0%; Pred. No. 9.2e-86; 1.1ve 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                 121 TLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 170
                                                                                                                                                                                                                                                                                                            300 tlpvefkcpdgevmkknmmfiktcachyncpgdndifeslyyrkmygdma 349
                                                                Disclosure; Column 15-18; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         Connective tissue growth factor (CTGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "signal peptide"
22.349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  AAW81425 standard; Protein; 349 AA
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95US-0386680.
95US-0459717.
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UNIV SOUTH FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                  Matches 170; Conservative
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         1999-384720/32
                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                     349 AA;
                   N-PSDB; AAX61317
                                               atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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14-DEC-1993;
10-FEB-1995;
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                                                                                                                                                     Sequence
                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
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factor (CTGF). This can be used in the method of the invention for inducing bone or tissue formation that comprises administration to a patient, a composition comprising CTGF and a carrier. CTGF can also be used in a method for inducing wound healing. The methods can be used for inducing bone, tissue or cartilage formation in disorders such as osteoporosis, osteoarthritis or osteochondrytis, arthritis, skeletal disorders, hypertrophy, or in wound healing. The CTGF and functional fragments are more stable and less susceptible to protease degradation than platelet derived growth factor (PDGF) and other growth factors known to be involved in wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 rpceadleenikkgkkcirtpkiskpikfelsgctsmktyrakfcgvctdgrcctphrtt 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 aayrledtfgpdptmiranclvqttewsacsktcgmgistrvtndnascrlekgsrlcmv 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
                                                                                                                                                                                                                                                                                                                                                     This represents the amino acid sequence of connective tissue growth
                                                                                                                                                                        e of connective tissue growth factor - for inducing bone, tissus cartilage formation in a patient or for inducing wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 948; DB 20;
; Pred. No. 9.2e-86;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                 Disclosure; Fig 1C; 30pp; English.
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100.0%;
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98US-0112241.
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Best Local Similarity 100.
Matches 170; Conservative
                                                           WPI; 1999-023382/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 AA;
                                                                                                     N-PSDB; AAV65380
Grotendorst GR;
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99WO-US29654
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Best Local Simi]
Matches 170; C
     14-DEC-1999;
                                       14-DEC-1998;
                                                       14-DEC-1998;
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         δy
                                                                                                                                                                                                              This sequence represents a human connective tissue growth factor (CTGF) collagen synthesis and/or myofibroblast differentiation. The invention of collagens to fragments of crofer, especially those encoded by exons 2 and/or fragments and the inductive activity. The protein and/or fragments of can be used to raise antibodies and the coding sequence can be used to can be used to raise antisense or disorder such as a fibrophylicative disease corresponding to treat a gainst the CTGF sequence can be used in a method to treat a spanial treation or disorder such as a fibrophylicative disease or disorder such as a fibrophylicative corresponding to the condition or disorder from kidney fibrosis, scleroderma, or disorders, andiogenesis, arthritis, hypertropic scarring, alther fibrosis, arthritis, hypertropic scarring, canherosclerosis, diabetic nephropathy and retrophylication disorders, skin fibrotic andiation therapy, and fibrosis of organs, disease or disorder can adiation therapy, and fibrosis of organs, diseases caused by vascular candiation therapy, and fibrosis of organs, diseases caused by vascular endothelial cell proliferation or migration (including cancers), endothelial cell proliferation or migration (including cancers), interstitial disease, dermatological diseases, diabetes, and keroids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; connective tissue growth factor; CTGF; mitogen; antibody; liver; fibroproliferative disease; scleroderma; fibrosis; kidney; arthritis; hypertropic scarting; atherosclerosis; diabetic nephropathy; retinopathy; hypertrepic scarting; atherosclerosis; wound healing; bone repair.
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                                                                                               Fragment of connective tissue growth factor, useful for treating fibroprollferative diseases or disorders, including kidney fibrosis, scleroderma, arthritis, hypertropic scarring, atherosclerosis, diabetic nephropathy and retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRIT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAYRLEDIFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
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100.0%; Score 948; DB 21; Length 349;
Best Local Similarity 100.0%; Pred. No. 9.2e-86;
Matches 170; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human connective tissue growth factor protein.
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                                                                                                                                                                                                 Claim 2, 3; Fig 3A-B; 74pp; English.
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                                                                 WPI; 2000-431565/37.
N-PSDB; AAA11278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 AA;
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                                   Grotendorst GR;
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Connective tissue growth factor; CCN growth regulator; anglogenesis; entianglogenic; basic fibroblast growth factor; bFGF; neovascular; entianglogenic; letthramis; all memangloma; letthramis; metastasis; prorisasis; tumour; glaucoma; diabetic retinopathy; arthritis; endometrisosis; Insulin-like growth factor-binding domain; IGF; von Willebrand factor type C repeat; Thrombospondin type 1 domain; C-terminal cysteine knot profile; CTCK-2; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a human connective tissue growth factor (CTGF) polypeptide which has mitogenic activity. The protein can be used to raise antibodies which specifically bind to CTGF and are used to treat a cTGF-associated disease or disorder, e.g. a fibroproliferative disease/disorder such as kidney fibrosis, scleroderma, pulmonary fibrosis, liver fibrosis, arthritis, hypertropic scarring, atherosclerosis, diabetic nephropathy and retinopathy, hypertension, kidney disorders, and cardiovascular disorders. The protein is also useful in wound healing, bone and tissue repair.
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                                                                                                                                                                                                                                                New fragment of connective tissue growth factor (CTGF) polypeptide having mitogenic activity, useful in wound healing, bone and tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 948; DB 21; Length 349; 100.0%; Pred. No. 9.2e-86; Live 0; Mismatches 0; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human connective tissue growth factor.
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                                                                                                                                                                                                                                                                                                                                                               Claim 2, 3; Fig 2A-B; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX44755 standard; protein; 349
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98US-0112240.
98US-0112241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                   Neff TB;
                                                                                                    (FIBR-) FIBROGEN INC.
                                                                                                                                                                                                WPI; 2000-431568/37.
N-PSDB; AAA11280.
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                                                                               (UYMI-) UNIV MIAMI
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                                                                                                                                                      Grotendorst GR,
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10-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                human CTGF.
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                                                                                                                                                                         The present sequence is human connective tissue growth factor, which is a member of CCN growth regulator family. It has antiangiogenic activity and is a potent inhibitor of basic fibroblast growth factor (bFGF)-stimulated bovine endothelial cell proliferation. It contains insulin-like growth factor (IGF)-binding domain, von Willebrand factor type C repeat, Thrombospondin type I domain and C-terminal cysteine knot profile (CTCK)-2 domain. It can be used to treat conditions associated with abnormal angiogenesis or neovascularisation like, retinal neovascularisation, tumour growth, haemangioma, solid tumours, leukaemia, metastasis, psoriasis, neovascular glaucoma, diabetic retinopathy, arthritis, endometriosis and premature retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human CTGF; connective tissue growth factor; recombinant production;
mitogenic; chemoterit; tissue development; growth; repair;
wound healing; vulnerary; diagnostic agent;
cellular proliferation disorder.
                                                                                                                                                                                                                                                                                                                                                                                            New anti-angiogenic protein containing an IGF binding, Willebrand factor type C, thrombospondin type 1 and cysteine knot domains is useful for inhibiting atopic angiogenesis e.g. in solid tumors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human connective tissue growth factor (CTGF).
                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                         Claim 6; Page 26-27; 30pp; English.
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                                                   CHIL-) CHILDRENS MEDICAL CENT
          99WO-US13338
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                              98US-0119804
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                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 170; Conservative
                                                                                           WPI; 2000-182688/16.
                                                                       Lin J;
          11-JUN-1999;
                              21-JUL-1998;
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                                                                       Folkman J,
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                                                                                                                                                                                                                                                                                                                                                                                Producing connective tissue growth factor involves transforming a host cell with polynucleotide encoding the growth factor and growing the cell under optimum conditions so that the polynucleotide is expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 948; DB 22; 100.0%; Pred. No. 9.2e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human connective tissue growth factor (CTGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Column 17-20; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB48831 standard; Protein; 349
95US-0386680
                                91US-0752427.
96US-0712302.
                                                                                                                                                                                                        Grotendorst GR, Bradham DM;
                                                                                                                                   (UYSF-) UNIV SOUTH FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                      WPI; 2001-210379/21.
N-PSDB; AAF59954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity
Matches 170; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence, 349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                 11-SEP-1996;
                                    30-AUG-1991;
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The invention relates to methods of accelerating wound healing in a patient. One method involves contacting the site of the wound with a patient. One method involves contacting the site of the wound with a composition comprising promise tissue growth factor composition comprising prowing growth factor beta (TGF-beta), which (TGF AAB48813) and transforming growth factor beta (TGF-beta), which still a the production of CTGF in vivo. Another method involves still a the growth of connective tissue cells by contacting the growth of connective thereof. CTGF is produced by cells with CTGF or an active fragment thereof. CTGF is produced by cells it has biologically similar activity to PDGF (platelet-derived site of a wound, and is also immunologically related to it, but it is growth factor), and is also immunologically related to it, but it is growth factor) and is also immunologically size tissue cells. CTGF, or healing by stimulating the growth of connective tissue cells. CTGF, or is functional fragments, is more stable and less susceptible to involved in wound healing. The present sequence represents human CTGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
                                                                                                                                                                                                                        Accelerating wound healing or stimulating growth of connective tissue cells involves contacting the site of a wound or cells with a composition comprising purified connective tissue growth factor and transforming growth factor beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fuman; monoclonal antibody; connective tissue growth factor; CIGF;
cell proliferation disorder; fibrosis; liver cirrhosis; nephritis;
skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer;
rheumatic vascular inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 948; DB 22;
; Pred. No. 9.2e-86;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat connective tissue growth factor.
                                                                                                                                                                                                                                                                                                                 Claim 1; Column 17-20; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY24379 standard; Protein; 347
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ilarity 100.08;
Conservative 0
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                                               93US-0167628.
95US-0386680.
96US-0712302.
91US-0752427.
                                                                                                                                                           Grotendorst GR;
                 98US-0097179
                                                                                                                              SOUTH FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                             WPI; 2001-079389/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 AA;
                                                                                                                                                                                                              N-PSDB; AAC87517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Sim
Matches 170;
                                                                                                                                 (UYSF-) UNIV
                                                                                                                                                                 Bradham DM,
                                                                                                  30-AUG-1991;
                       12-JUN-1998;
                                                      14-DEC-1993;
                                                                    .0-FEB-1995;
                                                                                     11-SEP-1996;
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connective tissue growth factor (GTGF). AAY24369 to AAY24378 represent connective tissue growth factor (GTGF). AAY24369 to AAY24378 represent these monoclonal antibodies. The antibodies are useful in the diagnosis, prevention and treatment of cell proliferation disorders in which GTGF is implicated, including fibrosis of lung, kidney, liver and other tissues; liver cirrhosis; nephritis; skin ulcers and keloid; rheumatoid arthritis; rheumatic vascular inflammation; hepatitis; and cancer. The present sequence represents rat GTGF.
                                                                                                                                                                                                                                                                         AAX90020 to AAX90029 encode monoclonal antibodies which react with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFGGVCTDGRCCTPHRTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AAYRLEDIFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transforming growth factor beta; induced; CEF-10; v-src; chicken; embryo; fibroblasts; TGF-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                New monoclonal antibody reactive with connective tissue growth factor useful in the treatment of cell proliferation disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TLPVEFKCPDGEVMKKNNMFIKTCACHYNCPGDNDIFESLYYRKWYGDMA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 tlpvefkcpdgeimknmmfiktcachyncpgdndifeslyyrkmygdma 347
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 926; DB 20;
Pred. No. 1.4e-83;
5; Mismatches 2;
                                                                                                                                                          Tamatani T, Tezuka
                                                                                                                                                                                                                                                          Claim 60; Page 167-169; 212pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR25566 standard; Protein; 348 AA
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                                                                                                   98JP-0356183
                                                                                                                97JP-0367699
                                                                           98WO-JP05697
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 95.9
Matches 163; Conservative
                                                                                                                                      (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                               Sakamoto S, Takigawa M,
                                                                                                                                                                                       WPI; 1999-430232/36.
N-PSDB; AAX90030.
                                                                                                                                                                                                                                                                                                                                                                                                  347 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beta-IG-M2
                                                                                                      15-DEC-1998;
25-DEC-1997;
                                W09933878-A1
                                                       08-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR25566;
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Screening actuation sequence with two probes from untreated with TGF-betal and cyclohexamide with two probes from untreated AKR-2B mouse cells induced with TGF-betal and cyclohexamide with two probes from untreated AKR-2B mRNA and AKR-2B mRNA from cells treated with cyclohexamide and TGF-betal.

Detal. The proteins encoded by hybridising colonies (beta-IG-M1 and beta-IG-M2) contain 38 Cys residues and are induced by TGF-betal.

Deta-IG-M2 included by various from the GCGCXXC motif reported in the manno half of insulan-like growth factor (IGF) binding proteins.

The C-terminal Cys rich region of beta-IG-M1, -M2 and CEF-10 contain an amino acid sequence with strong homology to a motif found near the C-terminal of the malarial circumsporozoite (CS) protein, which is criminal circumsporozoite (CS) protein, which is chighly conserved among all species of malarial parasites sequenced to date (designated region II). This motif is also found in other proteins which have cell addressive properties that mediate cell-cell and cell-extracellular matrix interactions, such as properdin, thrombospondin, and TRAP. The proteins encoded by TGF-beta induced genes are likely to be involved in mediation of the biological effects of TGF-beta relating to cell growth and differentiation. See also AAR25565.
                                                                                                                                                                                                                                                                                                                                                                    protein sequence was deduced from the DNA sequence obtd. by
                                                                                                                                                                                                                                                  TGF-beta induced gene family - encodes proteins involved in growth and differentiation effects of TGF-beta-1
                                                                                                                                       Neubauer MG, Purchio AF;
                                                                                       (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                       Claim 3; Fig 2; 35pp; English
                   91US-0642991.
                                                                                                                                  Brunner AM, Chinn J,
                                                                                                                                                                               WPI; 1992-243508/30.
                                                                                                                                                                                                       N-PSDB; AAQ26422
                     18-JAN-1991;
                                          10-JAN-1992;
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1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60 ó Query Match

97.7%; Score 926; DB 13; Length 348;
Best Local Similarity 95.9%; Pred. No. 1.4e-83;
Matches 163; Conservative 5; Mismatches 2; Indels ö

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61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120 g ò

121 TLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 170 ò

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Search completed: August 20, 2001; 22:46:28 Job time: 2504 sec

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1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
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                                                                                                         1 AAYRLEDTFGPDPTMIRANC......PGDNDIFESLYYRKMYGDMA 170
                                                        ; Search time 72.24 Seconds
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-712-302-2
US-08-880-031-2
US-09-054-368-2
US-09-054-179-2
US-09-054-274-2
US-09-080-715-2
US-09-056-704-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-760-797A-1
                                                                                                                                                   197339 seqs, 20590346 residues
                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                         US-09-461-646-2_COPY_180_349
948
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Listing first 45 summaries
                                       OM protein – protein search, using sw model
                                                       August 20, 2001, 22:06:59
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08468847B
Fatent No. 5780263
GENERAL INFORMATION:
APPLICANT: Hastings, Gregg A. and Adams, Mark D.
TITLE OF INVENTION: Human CCN-Like Growth Factor
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN,
ADDRESSEE: CECHHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
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Pred. No. 4.3e-83;
; Mismatches 0;
US-08-957-063-16
US-09-188-930-183
US-08-799-173A-13
US-07-862-021B-20
PCT-US93-03164-20
US-08-313-288B-12
US-08-313-288B-12
US-08-313-288B-12
US-08-908-526-8
                                                                                                                                                                                                                                                                                                                 US-08-820-170A 34
US-09-055-699 34
US-09-131-667-14
US-08-313-288B-18
US-07-862-021B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US93-03164-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATE:
FILING DATE: 6 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325800-442
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
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ATORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32580
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

Best Local Similarity 100.0%;

Matches 170; Conservative 0
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OPERATING SYSTEM: M
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FILING DATE:
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RESULT 3
US-08-386-680-2
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           239 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 298
                                                                                                                   61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 170
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                                                                                                                                                                                                                                                                                                   299 ILPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Grother Gary R.
APPLICANT: Grotherndorst, Gary R.
APPLICANT: Grotherndorst, Connective Tissue Growth Factor Title Of Invention: Connective Tissue Growth Factor NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Spensley Horn Jubas & Lubitz
ADDRESSE: Spensley Horn Jubas & Lubitz
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION ON THE SPLICATION ON THE SPLICATION OF THE SPLICATI
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-167-628-2
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US-08-167-628-2
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61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
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APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                        APPLICANT: Grotenorst, Gary R.
APPLICANT: Grotenorst, Gary R.
APPLICANT: Grotenorst, Bradham Jr., bouglas M.,
APPLICANT: Bradham Jr., bouglas M.,
APPLICANT: Bradham Jr., bouglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
TITLE OF INVENTION: CONNECTIVE SEQUENCES:
CORRESPONDENCES: AppReSS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
APPREST: A225 Executive Square, Suite 1400
CITY: La Jolla
STREET: La Jolla
STREET: La JOLLA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Fidopy disk
MEDIUM TYPE: Fidopy disk
COMPUTER: Fidopy disk
COMPUTER: PAGE COMPATIBLE
COMPUTER: PAGE COMPATIBLE
SUFTWARE: PAGE COMPATIBLE
CURRENT APPLICATION DATA:
FILING DATE: 10-FEB-1995
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
APPLICATION NUMBER: US/08/167,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Wetherell, Jr. Ph.D., John W. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
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Patent No. 5770209
GENERAL INFORMATION:
Sequence 2, Application US/08386680; Patent No. 5585270; GENERAL INFORMATION:
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TELEPHONE: 619-455-510
TELEFAX: 619-455-5110
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 170; Conservative
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APPLICATION NUMBER:
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CITY: La Jolla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
WUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATIS: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
STATE: La Jolla
STATE: CA
3: Spensley Horn Jubas & Lubitz
4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                 CUSTRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/459,717
CLASSIFCATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/752,427
FILING DATE: 30-AuG-1991
ATTORNEY. AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Patent No. 5783187
GENERAL INFORMATION:
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 170; Conservative
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                                                                                           ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-459-717-2
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                                     La Jolla
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 ADDRESSEE:
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                                                                             COUNTRY:
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                                       CITY:
STATE:
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240 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 299
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; Pred. No. 4.3e-83;
0; Mismatches 0; Indels
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APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Spensley Horn Jubas & Lubitz 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, '1r. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEPRAX: 619-455-5110
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NAME: Wetherell, Jr. Ph.D., John W.
US/08/712,302
                                                                                           us 08/386,680
                                                                                                                                           US/08/167,628
                                                                                                                                                                                        APPLICATION NUMBER: US/07/752,427 FILING DATE:
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APPLICATION NUMBER: US/08/167,628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08880031; Patent No. 5916756; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
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Best Local Similarity 100.0%;
Matches 170; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 2:
               FILING DATE: 11-SEP-1996
CLASSIFICATION: 435
                                                                                                                    10-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 amino acids
                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 10-FEB-19
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-712-302-2
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MEDIUM TYPE: Floppy
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APPLICANT: University of South Florida
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COUNTRY:
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CITY: La
                  RESULT 8
US-09-097-179-2
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GENERAL INFORMATION:
APPLICANT: University of South Florida
APPLICANT: University of South Florida
APPLICANT: Bradham, Jr., Douglass M.
APPLICANT: Bradham, Jr., Douglass M.
APPLICANT: Bradham, Jr., Douglass M.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
FILE REFERENCE: 07414/003005
CURRENT FILING DATE: 1998-04-02
EARLIER APPLICATION NUMBER: 08/459,717
EARLIER FILING DATE: 1995-06-02
EARLIER FILING DATE: 1995-06-02
EARLIER FILING DATE: 1995-06-02
EARLIER FILING DATE: 1993-12-14
NUMBER: OF SEQ ID NOS: 9
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100.0%; Pred. No. 4.3e-83;
tive 0; Mismatches 0;
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 REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5110
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
31,678
                                                                                                                    : 349 amino acids amino acid
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Best Local Similarity 100.
Matches 170; Conservative
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US-09-054-368-2
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Best Local Similarity
Matches 170; Conserv
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61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
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                                                 APPLICANT: Grotendorst, Gary R.
APPLICANT: Grotendorst, Gary R.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE PATENTIN RELEASE #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/097,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 948; DB 4;
ilarity 100.0%; Pred. No. 4.3e-83;
Conservative 0; Mismatches 0;
                                                                                                                                 SEEE: Spenaley Horn Jubas & Lubitz
F: 4225 Executive Square, Suite 1400
La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Wetherell, Jr. Ph.D., John W. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,680
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US/08/167,628
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/07/752,427
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; Patent No. 6150101
Sequence 2, Application US/09097179 Patent No. 6149916 GENERAL INFORMATION:
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TELEPHONE: 619-455-5100
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ATTORNEY/AGENT INFORMATION:
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amino acid
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Best Local Similarity
Matches 170; Conserv
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61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
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TITLE OF INVENTION: METHODS OF DIAGNOSING A PATHOLOGY
TITLE OF INVENTION: METHODS OF DIAGNOSING A PATHOLOGY
TITLE OF INVENTION: CHARACTERIZED BY A CELL PROLIFERATIVE
TITLE OF INVENTION: DISORDER ASSOCIATED WITH CONNECTIVE
TITLE OF INVENTION: TISSUE GROWTH FACTOR (Amended)
FILE REFERENCE: 07414/003002
CURRENT APPLICATION NUMBER: US/09/056,704
CURRENT FILING DATE: 1998-03-03
EARLIER FILING DATE: 1995-06-10
EARLIER APPLICATION NUMBER: 08/459,717
EARLIER FILING DATE: 1995-06-02
EARLIER APPLICATION NUMBER: 08/167,628
EARLIER FILING DATE: 1993-12-14
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASTSEQ for Windows Version 4.0
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Best Local Similarity 100:0%; Pred. No. 4.3e-83;
Matches 170; Conservative 0; Mismatches 0:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09056704 Patent No. 6232064 GENERAL INFORMATION:
REFERENCE/DOCKET NUMBER: PI
TELECOMONICATION INFORMATION
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
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Conservative (
                                                                                                                                                 349 amino acids
                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acid
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US-09-056-704-2
                                                                                                                                                                      amino acid
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; MOLECULE TYPE:
US-09-080-715-2
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            APPLICANT: Braden, Jr., Douglass M.
TITLE OF INVENTION: METHODS OF IDENTIFYING A COMPOSITION
TITLE OF INVENTION: HATA ALTERS CONNECTIVE TISSUE GROWTH
TITLE OF INVENTION: PACTOR EXPRESSION (Amended)
FILE REFERENCE: 07414/003004
CURRENT APPLICATION UNMBER: US/09/054,274
CURRENT FILING DATE: 1996-04-02
EARLIER APPLICATION NUMBER: 08/386,680
EARLIER APPLICATION NUMBER: 08/459,717
EARLIER APPLICATION NUMBER: 08/459,717
EARLIER APPLICATION NUMBER: 08/167,628
EARLIER APPLICATION NUMBER: 08/167,628
EARLIER PILING DATE: 1993-12-14
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASELSO FOR WINDOWS VERSION 4.0
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APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 948; DB 4;
100.0%; Pred. No. 4.3e-83;
ilve 0; Mismatches 0;
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4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      John W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
APPLICATION NUMBER: US/07/752,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/080,71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09080715 Patent No. 6190884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: La Jolla
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US-09-080-715-2
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TOPOLOGY: LINEAR MOLECULE TYPE: PROTEIN
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: USA
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NEW JERSEY
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               USA
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 STATE: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 349;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/08468847B
; Sequence 15, Application US/08468847B
; Sequence 15, Application US/08468847B
; Patent No. 5780263
; CENERAL INFORMATION:
APPLICANT: Hastings, Gregg A. and Adams, Mark D. APPLICANT: Hastings, Gregg A. and Adams, Mark D. APPLICANT: Hastings. 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk COMPUTER: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US96/08140 FILING DATE: 30-MAY-1996 CLASSIFLATION:
                                                                                                    Sequence 2, Application PC/TUS9608140
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: University of South Florida
TITLE OF INVENTION:
CONRESPONDENCE: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 948; DB 5;
Best Local Similarity 100.0%; Pred. No. 4.3e-83;
Matches 170; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07414/003WO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION UNDRER: 38.347
REFERENCE/DOCKET NIMBER: 07414
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEPAX: 619-678-5079
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein
PCT-US96-08140-2
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61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 TLPVEFKCPDGEIMKNNMFIKTCACHYNCPGDNDIFESLYYRKWYGDMA 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 926; DB 1; Length 348;
Pred. No. 5.4e-81;
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US-08-468-847B-16
Sequence 16, Application US/08468847B.
Patent No. 5780263
GENERAL INFORMATION:
APPLICANT: Hastings, Gregg A. and Adams, Mark D. APPLICANT: Hastings, Cregg A. and Adams, Mark D. APPLICANT: Hastings, Cregg A. and Adams, Mark D. APPLICANT: Human CCN-Like Growth Factor UNDER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSES: CARELLA, BYRNE, BAIN, GILFILIAN, ADDRESSES: CACCHI, STEWART 6 OLSTEIN
STREET: 6 BECKER FARM ROAD
CONTY: ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
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6 June 1995
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2 INCH DISKETTE
SOFTWARE: WORD PERRECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,847B
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORIEY AGENT INFORMATION:
NAME: MULLING, J.G.
REGISTATION NUMBER:
REGISTATION NUMBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33,073
pp. 325800-442
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
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SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 95.9%;
Matches 163; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       57.0%; Score 540.5; DB 1; Length 351; 59.9%; Pred. No. 3.3e-44; Live 22; Mismatches 40; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-08-468-8478-17
Sequence 17, Application US/08468847B
Setent No. 5780263
GENERAL INFORMATION:
APPLICANT: Hastings, Gregg A. and Adams, Mark D.
TITLE OF INVENTION: Human CCN-Like Growth Factor
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIF 157
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ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-442
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1704
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
LENGTH: 351 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      325800-442
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FILING DATE: 6 June 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 33,073
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 59.99
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
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USA
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CITY: ROSELAND
STATE: NEW JERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07068
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                                                                                                                                                                                                                                                                                                                                                                                                                              2; Gaps
                                                                                                                                                                                                                                                                                                                 1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 TTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIF-ESLYYRKMYGDM 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 357;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                    51;
                                                                                                                                                                                                                        54.3%; Score 515; DB 1; 54.4%; Pred. No. 9.2e-42;
                                                                                                                                                                                                                                                                    25; Mismatches
INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
                                            LENGTH: 357 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                                                                                                                        Query Match 54.3%
Best Local Similarity 54.4%
Matches 93; Conservative
                                                          TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-468-847B-17
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Search completed: August 20, 2001, 22:47:51 Job time: 2452 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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- protein search, using sw model OM protein August 20, 2001, 22:43:25 ; Search time 75.11 Seconds Run on:

(without alignments)
172.409 Million cell updates/sec

US-09-461-646-2\_COPY\_180\_349 948 Title: Perfect

score:

1 AAYRLEDTFGPDPTMIRANC......PGDNDIFESLYYRKMYGDMA 170 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\* 1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S	Description	connective tissue	beta IG-M2 protein	NOV protein - chic	gene novH protein	CYR6	0 prot	hypothetical prote		protein CTRP - mal	F-spondin - rat	immunodominant mic	F-spondin precurso	LDL-receptor-relat	hypothetical prote	hypothetical prote	z	cysteine rich prot	hypothetical prote	hypothetical prote	mucin 5AC (clone L	hypothetical prote	probable tenascin	circumsporozoite p	thrombospondin pre	hypothetical prote	metallothionein-2	secreted leucine-r	otogelin - mouse	circumsporozoite p
SUMMARIES	ID	A40551	A40578	S20078	138069	A35669	A41428	T21371	T18856	T18397	A38152	A45638	A47723	A47437	T29247	T14764	T18517	T42017	T22545	T19477	A57534	T25933	T09070	A39756	A39804	T34395	S50911	T42626	T42214	OZZQAF
	DB	7	~	~	7	7	7	~	~	~	~	7	~	Н	~	~	~	7	7	7	7	7	7	~	~	ď	7	~	~	Н
	Length	349	348	351	357	379	375	2165	1444	2098	807	712	803	4753	654	868	1205	1274	1059	651	1042	1372	4006	388	1178	2167	104	1025	2910	412
ф	Query Match	100.0	7.76	57.0	54.3	51.4	50.6		11.3	•	10.7	10.4	10.4	10.2	10.2	10.2	9.7	9.7	•		•	9.5		9.4	9.4	9.4	9.3	9.3	٠	9.5
	Score	948	926	540.5	515	487.5	479.5	116	101	102.5	101.5	66	66	97	96.5	96.5	92	92	91	90.5	90.5	90.5			89.5	88	88.5	88	88	87.5
	Result No.		7	e	4	2	Q	7	80	σ	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	. 26	27	28	.29

circumsporozoite p	circumsporozoite p	hypothetical prote	high-sulfur wool m	finger protein HZF	mucin-like peptide	thrombospondin 1 p	circumsporozoite p	hypothetical prote	thrombospondin 1 p	antigen Em100 - Ei	hypothetical prote	keratin high-sulfu	high-sulfur wool m	high-sulfur wool m	hypothetical prote
A54533	A54529	T15976	147109	S47073	A42112	TSHUP1	JC6164	T00260	A40558	A48569	T34565	KRSHHC	147112	147105	T16840
~	~	7	7	~	~	Н	7	~	7	7	7	Н	N	~	7
424	442	957	152	732	837	1170	388	951	1170	724	111	152	152	182	1101
9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.1	9.1	9.1	9.0	9.0	9.0	0.6	9.0	0.6
87.5	87.5	87.5	87	87	87	87	86	86	98	85.5	85	85	82	85	82

## ALIGNMENTS

RESULT

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A. Cell Biol. 114, 1283-12494, 1291
A. Title: Connective tissue growth factor: a cysteine-rich mitogen secreted by human v A;Reference number: A40551; MUID:91373462
A;Reference number: A40551; MUID:91373462
A;Residues: 1349 < BRA>
A;Residues: 1349 < BRA>
A;Residues: 1349 < BRA>
A;Cross references: GB:M92934; GB:M36965; GB:S56201; NID:g180923; PIDN:AA91279.1; PI B;Oemar, B.S.; Werner, A.; Yang, Z.; Garnier, J.M.; Gentz, R.; Luescher, T.F.
Submitted to the EMBL Data Library, April 1994
A;Reference number: S44205
A;Reference number: S44205
A;Accession: S44205
A;Accession: S44205
A;Accession: S44205
A;Accession: By preliminary
A;Accession: By
                                                    C;Species: Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 170
                                                                                                                                                                                  C;Accession: A40551; S44205
R;Bradham, D.M.; Igarashi, A.; Potter, R.L.; Grotendorst, G.R.
J. Cell Biol. 114, 1285-1294; 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 94%; DB 2; Best Local Similarity 100.0%; Pred. No. 1.5e-75; Matches 170; Conservative 0; Mismatches 0;
connective tissue growth factor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
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Gaps

RESULT

beta IG-M2 protein precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 06-Mar-1992 #sequence\_revision 06-Mar-1992 #text\_change 01-Dec-2000 C;Accession: A40578; A53228 R;Brunner, A.; Chinn, J.; Neubauer, M.; Purchio, A.F. DNA Cell Biol. 10, 293-300, 1991 A;Title: Identification of a gene family regulated by transforming growth factor-beta A;Reference number: A40578; MUID:91229699

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A; Molecule type: mRNA
A; Residues: 1-379 < CABA
A; Cress references: GB:M32490; NID:g192909; PIDN:AAA37512.1; PID:g309206
A; Cress references: GB:M32490; NID:g192909; PIDN:AAA37512.1; PID:g309206
A; Note: the authors translated the codon GAT for residue 337 as Gln
A; Note: the authors translated the codon GAT for residue 337 as Gln
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A; Tatle: Promoter function and structure of the growth factor-inducible immediate ear
A; Reference number: 148319; MUID:91288203
gene novH protein - human
C;Species: Homo sapiens (man)
C;Decies: 17-May-1996 #sequence_revision 17-May-1996 #text_change 05-Nov-1999
C;Date: 17-May-1096 #sequence_revision 17-May-1996 #text_change 05-Nov-1999
C;Accession: 138069
R;Martinerie, C; Huff, V; Joubert, I.; Badzioch, M.; Saunders, G.; Strong, L.; Perb
Oncogene 9, 2792-2732, 1994
A;Title: Structural analysis of the human nov proto-oncogene and expression in Wilms
A;Reference number: 138069; MUID:94336229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene CYR61 protein precursor - mouse gene CYR61 protein precursor - mouse gene CS precies: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 05-Nov-1999
C; Date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 05-Nov-1999
C; Accession: A3569; 148319; S16446
A; Reference number: A3569; MUID:90287146
A; Reference number: A35669.
A; Accession: A35669.
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RPCEADLEE-NIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X78351; NID:9587422; PIDN:CAA55146.1; PID:9825696
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAYRLEDIFGPDPTMIRANCLVQTTFWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Status: translated from GB/EMBL/DDBJ
A.Status: translated bNA
A.Molecule type: DNA
A.Molecule type: 1-379 <RES>
A.Gross-references: EMBL:X56790; NID:g50632; PIDN:CAA40109.1; PID:g5
A.Gross-references: EMBL:X56790; NID:g50632; PIDN:CAA40109.1; PID:g5
A.Gross-references: EMBL:X56790; NID:g50632; PIDN:CAA40109.1; PID:g5
A.Note: the authors did not translate the codon GAT for residue 337 as Gln
A.Note: the authors translated the codon GAT for residue 337 as Gln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 TTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIF-ESLYYRKMYGDM 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                 A;Introns: 28/3; 104/1; 188/1: 259/3
A;Introns: 28/3; thrombospondin type 1 repeat homology
C;Superfamily: thrombospondin type 1 repeat homology <THR1>
F;203-250/Domain: thrombospondin type 1 repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 487.5; DB 2;
Pred. No. 2.4e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.3%; Score 515; DB 2;
54.4%; Pred. No. 9.2e-38;
11ve 25; Mismatches 51.
                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-357 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 54.34
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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C;Bate: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Bate: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Bate: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2007
C;Batession: $20078
R;Jule: Proviral rearrangements and overexpression of a new cellular gene (nov) in myel A;Reference number: $20078; MuID:92107157
A;Recession: $20078
A;Status: preliminary
                                                                                                                                           A;Cross-references: GB:M80263; NID:g201945; PIDN:AAA73135.1; PID:g201946
R;Ryseck, R.P.; Macdonald-Bravo, H.; Mattei, M.G.; Bravo, R.
Cell Growth Differ. 2, 225-233, 1991
A;Title: Structure, mapping, and expression of fisp-12, a growth factor-inducible gene A;Reference number: A53228; MUID:91363290
A;Accession: A53228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-351 <JUD>
A;Cross-references: EMBL:X59284; NID:g63702; PIDN:CAA41975.1; PID:g63703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAYRLEDIFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-160, K',162-348 <RYS>
A;Residues: 1-160, K',162-348 <RYS>
C;Genetics: C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 926; DB 2; Length 348;
pred. No. 1.2e-73;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40;
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59.9%; Pred. No. 5.4e-40;
Live 22; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ILPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . |: |||:|| |: :|| || || || || || || ||: |
302 TIQVEFRCPGGKFLKKPMMLINTCVCHGNCPOSNNAF 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.7%;
ilarity 95.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94; Conservative
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Best Local Similarity
Matches 94; Conserv
                                                                             A, Accession: A40578
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-348 < CRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Sim
Matches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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A; Gene: NOV
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138069
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5

Gaps

3

Gaps

6

44; Indels

32; Mismatches

83; Conservative

Matches

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A;Gene: CESP:F25H8.3
A;Map position: 4
A;Introns: 31/1; 52/1; 135/2; 193/3; 216/1; 266/1; 495/2; 547/3; 584/3; 634/2; 744/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Matches 29; Conserv
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A;Molecule type: DNA
A;Residues: 1-2165 <WI2>
A;Cross-references: EMBL:269361; PIDN:CAA93288.1; GSPDB:GN00022; CESP:F25H8.3
A;Experimental source: clone T13H10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: Maria A4128
F.Stimmons, D.L.; Levy, D.B.; Yannoni, Y.; Erikson, R.L.
Proc. Natl. Acad. Sci. U.S.A. 86, 1178-1182, 1989
A.Title: Identification of a phorbol ester-repressible v-src-inducible gene.
A;Reference number: A41428
A;Reference number: A41428
A;Reference number: A1428
A;Refer
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C;Species: Caenorhabditis elegans
C;Spaces: 121371; 724896
R;Gajadsty, S.
Submitted to the EMBL Data Library, February 1996
A;Reference number: 219413
A;Reference number: 219413
A;Recession: T21371
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 1-2165 < WILD
A;Residues: 1-2165 < WILD
A;Residues: 1-2165 < WILD
A;Coss-references: EMBL:Z69360; PIDN:CAA93287.1; GSPDB:GN00022; CESP:F25H8.
A;Experimental source: clone F25H8
                                                                                                                                                                                                                                   66 DLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTTLPVE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270 PSYASLKKGKKCTKTKKSPSPVRFTYAGCSSVKKYRPKYCGSCVDGRCCTPQQTRTVKIR 329
                                                                   PCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTT 121
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                                   FGPDPTMI-----RANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB:J04496; NID:g211435; PIDN:AAA48661.1; PID:g211436
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                                                                                                                                                                                                                                                                                                                                           122 LPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDM 169
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submitted to the EMBL Data Library, February 1996
A;Reference number: 219949
A;Accession: T24896
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A41428
CEF-10 protein precursor - chicken
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A,Map position: X
A:Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3;
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                                                                    14;
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A;Residues: 1-1444 <MI2>
A;Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN00028; CESP:C02B4.1
A;Experimental source: clone T07C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-1444 <WIL>
A;Cross-references: EMBL:250004; PIDN:CAA90293.1; GSPDB:GN00028; CESP:C02B4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  angiogenesis inhibitor homolog - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                   1858 VPKEKCELFPKPNESQTCELNPCDSEFKWSFGPWGECSKNCGQGIRRRVKCV----AND 1913
                                                                                                                                                                                                                                                                                                                                                                                                                                            1914 GRRVERVKCTTKKPRRTQYC----FERNCLPSTCQELKSQNVKAKDGNYTILLDGFTIEI 1969
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                                                                                                                            13 PIMIR----ANCLVQTT--EWSACSKTCGMGISTRVT-----NDNAS-----------48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1970 YCHRMNSTIPKAYLNVNPRTNFAEVYGKKLIYPHTCPFNGDRNDSCH--CSEDGD 2022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 --HR-TTTLP-----VEFKCPDGEVMKKNMMFIKTC-----ACHYNCPGDND 155
                                                                    52; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
12.2%; Score 116; DB 2; Length 2165;
Best Local Similarity 21.3%; Pred. No. 0.031;
Matches 50; Conservative 31; Mismatches 52; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.3%; Score 107; DB 2; Length 1444; 26.1%; Pred. No. 0.13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein CTRP - malaria parasite (Plasmodium falciparum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, July 1995
A;Reference number: 219031
A;Accession: T18856
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, July 1995
A;Reference number: 219917
A;Accession: 724653
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                        49 ----CRL---EKQSRLCMVRPCEADLE------
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                                                                                                                                                                                                                                                                                                                                                                                     86 PIKFELSGCTSMKTYRAKFCGVCTDGRCCTP----
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A47723
A47723
C. Species: Xenopus laevis (African clawed frog)
C. Species: Xenopus laevis (African clawed frog)
C. Species: Z7-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Nov-2000
C. Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Nov-2000
C. Accession: A47723
R. Ruiz I Altaba, A.: Cox, C.: Jessell, T.M.: Klar, A.
R. Ruiz I Altaba, A.: Cox, C.: Jessell, T.M.: Klar, A.
A; Title: Ectopic neural expression of a floor plate marker in frog embryos injected w A; Reference number: A47723; MUID: 93376785
                                                                                                                                                                                                                                                                                                                           A, Status: preliminary
A, Status: preliminary
A, Status: preliminary
A, Status: preliminary
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-712 CTOM>
A, Residues: 1-712 CTOM>
A, Residues: 1-712 CTOM>
A, Residues: 1-772 (TOM)
A, Cross-references: GB. AF032905; GB: M73495; NID: g2707732; PIDN: AAD03350.1; PID: g27077
A, NOTE: sequence extracted from NCBI backbone (NCBIN: 77752, NOB Hilbbrand factor type 1 repeat homology vowAl>
F; 48-218/Domain: von Millebrand factor type A repeat homology CTHR1>
F; 38-296/Domain: thrombospondin type I repeat homology CTHR3>
F; 309-371/Domain: thrombospondin type I repeat homology CTHR4>
F; 494-556/Domain: thrombospondin type I repeat homology CTHR5>
F; 494-556/Domain: thrombospondin type I repeat homology CTHR6>
F; 560-610/Domain: thrombospondin type I repeat homology CTHR6>
                                                                                                                                                                 C; Accession: A45638
R; Tomley, F.M.; Clarke, L.E.; Kawazoe, U.; Dijkema, R.; Kok, J.J.
R; Tomley, F.M.; Clarke, L.E.; Kawazoe, U.; Dijkema, R.; Kok, J.J.
Mol. Biochem. Parasitol. 49, 277-288, 1991
A; Title: Sequence of the gene encoding an immunodominant microneme protein of Elmeria A; Reference number: A45638; MUID:92131064
A; Reference number: A45638; MUID:92131064
A; Recession: A45638
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A; Status: nRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-803 < RUI>
A; Cross-references: GB:L09123; NID:g409244; PIDN:AAA19105.1; PID:g409245
A; Cross-references: GB:L09123; NID:g409244; PIDN:AAA19105.1; PID:g409245
B; C; Superfamily: F-spondin; thrombospondin type 1 repeat homology < THR1>
F; 407-662/Domain: thrombospondin type 1 repeat homology < THR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunodominant microneme protein Etpl00 - Eimeria tenella
C;Species: Elmeria tenella
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 DPTMIRANCLVQTTEWSACSKTCGMGISTRVIN---DNA-----SCRLEK-----QSRL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                487 CNTOPCPVDEVVGDWEDWGQCSEQCGGGKRTRNRGPSKQEAMFGGKTVAQQNAELPEGEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.4%; Score 99; DB 2; Length 803; 26.8%; Pred. No. 0.39;
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Pred. No.
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24.0%;
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Best Local Si
Matches 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C;Date: 04-Mar-1993
C;Date: 04
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C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T18397
C;Accession: T18397
A;Title: Molecular cloning of a gene from Plasmodium falciparum that codes fo. A;Title: Molecular cloning of a gene from Plasmodium falciparum that codes fo. A;Title: Molecular cloning of a gene from GD/EMBL/DDBJ
A;Accession: T18397
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecular type: DM.
A;Cross-references: EMBL:U34363; NID:g1098897; PID:g1098898; PIDN:AAC46961.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1645 SDWSSCSKTCGYSTRSRTFTILPEYIGEYPNCKIFERSETEVCAFIPACSDENCFEWEEW 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GKKC-----IRTPKISKPIKFELSGCTSMKTYRAKFCG---VCTDGRC----- 113
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A,Status: preliminary
A,Status: preliminary
A,Status: preliminary
A,Roblecule type: mRNA
A,Robelcule type: mRNA
A,Robelcule type: mRNA
A,Robelcule type: mRNA
A,Robelcule type: mRNA
A,Cross-references: GB: W88469, NID: 9204176; PIDN: AAA11174.1; PID: 9204177
A,Cross-references: GB: W88469, NID: 9204176
A,Robelcule to an anti-prompospondin type I repeat homology CTHR2>
C,Superfamily: F-Spondin; thrombospondin type I repeat homology CTHR2>
F; 500-555/Domain: thrombospondin type I repeat homology CTHRA>
F; 557-611/Domain: thrombospondin type I repeat homology CTHRA>
F; 566/Domain: thrombospondin type I repeat homology CTHRA>
F; 567-721/Domain: thrombospondin type I repeat homology CTHRA>
F; 667-721/Domain: thrombospondin type I repeat homology CTHR5>
F; 657-807/Domain: thrombospondin type I repeat homology CTHR5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EWSACSKTCGMGISTRVTNDNA----SCRLEKQSRL--CMVRPCE----ADLEENIKK- 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2098;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 -----CIPHRITILPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDND 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 102.5; DB 2;
; Pred. No. 0.45;
21; Mismatches 52;
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Pred. No. 0.23;
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illarity 23.8%;
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les 42; Conserv
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Matches 40; Conserv
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A;Gene: CESP:F09F9.4
A;Introns: 89/3; 138/3; 192/3; 260/1; 312/1; 400/2; 445/3; 496/1; 523/1; 558/2; 596/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------ACRQGFMINKEN-NHSCQKDPAEKIEQLCSSNSTQFQCKN 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1066 GRCIPKEWKCDGENDCLDESDEIDEKGDKCFHETECAENTIKCRNTKKCIPAQYGCDGDN 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMKTYRAKFCGVCTDGR---C---CTPHRTTTLPVEFKCP-----DGEVMKKNMMF 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 TEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC---MVRPCEADLEENIKKGKKCIRTP 81
                                                                                                                                                                                                                                                                                                                                                                                             homology <EGF2> receptor YWTD-containing repeat homology <YW38>
                                               <LD22>
                                                                                                                                                                                                                                                                                                    <LD32>
                                                                                           <LD24>
                                                                                                                                                                                                           <LD28>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.2%; Score 97; DB 1; Length 4753; 21.8%; Pred. No. 2.9;
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A;Moleotule type: DNA
A:Residues: 1.654 <AINN
A;Cross-references: EMBL:U40958; PIDN:AAA81764.1; CESP:F09F9.4
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A;Description: The sequence of C. elegans cosmid F09F9,
A;Reference number: 220594
A;Accession: T29247
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Best Local Similarity
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R; Minx, P.; Hawkins, J.
                                                                                                                                      F;3627-3666/Domain:
F;3671-3705/Domain:
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                                                    .35/Domain:
                                                                       174/Domain:
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F;53-87,Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;92-131/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;138-175/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;138-175/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;23-277/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;262-297/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;262-297/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;302-336/Domain: EGF homology <EGFI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Yochem, J.; Greenwald, I. submitted to the EMBL Data Library, July 1992
A; Description: A gene for an LDL receptor-related protein (LPR) in the nematode C.elegan A;Reference number: $27801
A;Accession: $27801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 1
A;Introns: 31/1; 88/1; 132/1; 172/3; 219/1; 298/1; 463/2; 526/2; 585/3; 780/2; 874/2; 97
                                                                                                                                                                                                                                                                     RESULT 13
A47437
LDL-receptor-related protein - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Aug-2000
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
R.Yochem, J.; Greenwald, I.
Proc. Natl. Acad. Sci. U.S.A. 90, 4572-4576, 1993
A.Title: A gene for a low density lipoprotein receptor-related protein in the nematode A.Reference n.1...
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A;Readdues: 1-4753 <WLL>
A;Cross-references: EMBL:273907; PIDN:CAA98124.1; GSPDB:GN00019; CESP:F29D11.1
A;Experimental source: clone F29D11
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A; Residues: 11-4753 < YCC>
A; Cross-references: GB: M96150; NID:9156359; PIDN:AAA28105.1; PID:9156360
A; Note: nucleotide sequence not given; translation not complete in this paper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Molecule type: DNA
A; Mostagues: 1-4753 < YO2>
A; Residues: 1-4753 < YO2>
A; Cross-references: EMBL:M96150; NID:g156359; PIDN:AAA28105.1; PID:g156360
A; Wilkinson, J.
Submitted to the EMBL Data Library, June 1996
A; Reference number: 219439
A; Accession: T21547
A; Status: preliminary; translated from GB/EMBL/DDBJ
<YW33>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <LD11>
<LD12>
<LD13>
<LD14>
                                                                71 IKKGKKCIRTPKISKPIKFELSGCTSMKTYRA----KFCGVCTDGRCCTPHRTTTLPVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <LD17><LD18><LD19>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDL receptor ligand-binding repeat homology LDL receptor ligand-binding repeat homology
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                                                                                                                                                           126 FKCPDGEVMKKNMMFIKTCACH 147
                                                                                                                                                                                                       787 TSCKD----KKE---IRACNVH 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homology
receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;1101-1138/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;1146-1182/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;1187-1223/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1228-1263/Domain:
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F;2919-2956/Domain:
F;2961-2997/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;1270-1307/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;1313-1350/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1441-1475/Domain:
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10;

7;

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RESULT 15
Training the protein DKFZp434H204.1 - human (fragment)
hypothetical protein DKFZp434H204.1 - human (fragment)
C; Species: Homo saplens (man)
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999
R; Wanbutted, C, Hebbort, D; Mewes, H.W.; Gassenhuber, J; Wiemann, S.
R; Status: preliminary
A; Reference number: 21818
A; Referen
```

Search completed: August 20, 2001, 22:53:13 Job time: 588 sec

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GenCore version 4.5
Copyright (c) 1993'- 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 20, 2001, 22:47:55 ; Search time 57.66 Seconds (without alignments) 100.996 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-461-646-2\_COPY\_180\_349 948 1 AAYRLEDTFGPDPTMIRANC......PGDNDIFESLYYRKMYGDMA 170

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 Total number of hits satisfying chosen parameters: 93435 seqs, 34255486 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	homo	sns	P29268 mus musculu		P42642 coturnix co	P28686 gallus gall		P48745 homo sapien		P18406 mus musculu	homo s	gallus	7 gallus	rattus	_	Q04833 caenorhabdi					P35440 gallus gall			P56159 homo sapien		~		P13814 plasmodium			Q14586 homo sapien	308	P07996 homo sapien
SUMMARIES	QI	CTGF_HUMAN	CTGF_PIG	CTGF_MOUSE	CTGF_BOVIN	NOV_COTJA	NOV_CHICK	NOV_XENLA	NOV_HUMAN	NOV_MOUSE	CYR6_MOUSE	CYR6_HUMAN	CE10_CHICK	NRTR_CHICK	FSPO_RAT	FSPO_XENLA	LRP_CAEEL	NRTR_MOUSE	NRTR_HUMAN	ATS2_BOVIN	CSP_PLARE	TSP2_CHICK	TSP1_XENLA	MT1_TETPI	GDNR_HUMAN	GDNR_CHICK	NEL1_HUMAN	CSP_PLAFA	CSP_PLAFT	CSP_PLAFW	ATS2_HUMAN	Z267_HUMAN	MUCL_RAT	TSP1_HUMAN
	8 : B	Н.	⊶.	-	Н	-	~4	Н	Н	Н	П	П	Н	7	Н	<del>i</del>		Н		П	Н		~	-	7	Н	Н	Н	Н	7	н	-1	Н	Н
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iry	Match	0.	0		9	۲.	0.	. 7	۳.		7	7		.7	.7		. 2	σ.	6.	.,	4.	4.	4.	<u>.</u>	<u>س</u>	<u>ښ</u>	<u>ښ</u>			~	~	~	~	. 2
* Query	Mat	100	86	6	6,	5	5	54	2	5	5	5	Š	10	H	7	ĭ	O1	٥,	٥,	Ů,	٥,	٠,	6	٠,	٥,	Ų,	O1	5	σ,	o	o	o	01
	Score	948	929	926		◂		518.5	_					101.5		66	26	94	94		89.5	on.		88.5	∞ .	∞ .	æ	$\sim$	2	^	$\sim$	87	87	87
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Q28178 bos taurus P35441 mus musculu	P02440 ovis aries P19597 plasmodium Q95116 bos taurus	P09208 drosophila Q62919 rattus norv	014514 homo sapien P13671 homo sapien	P22105 homo sapien P98164 homo sapien	P98060 caenorhabdi
TSP1_BOVIN	KR2C_SHEEP CSP_PLAFO TSP2_BOVIN	INSR_DROME NEL1_RAT	BAI1_HUMAN CO6_HUMAN	TENX_HUMAN LRP2_HUMAN	TOH2_CAEEL
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1170	151 397 1170	2146	1584 934	4289	610
9.1	0 & & 0 0 0	8 8 6 8	8.8 8.7	8 8 6 6	8.5
8 8 9 8 9 8	84.5 84	84 83.5	83.5 82.5	82 81.5	81
34 35	36 37 38	39	41	<b>4</b> 3	45

## ALIGNMENTS

RESULT ALCO COLORD DDT O1-DB DDT O1-
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRETED BY HUMAN VASCULAR ENDOTHELIAL CELLS. THIS IMMEDIATE-EARLY PROTEIN MAY BIND ONE OF THE PDGF CELL SURFACE RECEPTORS.
-i- SUBUNIT: MONOMER (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN FAMILY. CEF-10/CYRÉL/OFTG/FISP-12/NOV PROTEIN SUBFAMILY.
-i- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (CTGF) (FISP-12 PROTEIN).
CTGF OR FISP12 OR FISP-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONNECTIVE TISSUE GROWTH FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 929; DB 1; Length 34
Pred. No. 5.3e-76;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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A; BB510E2B52D4A0 CRC64;
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PROSITE: PSO1185; CTCK_1; 1.
PROSITE: PSO1185; CTCK_2; 1.
PROSITE: PSO1185; CTCK_2; 1.
Growth factor binding; Signal, SIGNAL 1 26
CONNEC CHAIN 101 167 CONNEC CHAIN 256 233 CTCK_DOWAIN 256 233 CTCK_DOWAIN 256 293 BY SIP DISULFID 273 307 BY SIP DISULFID 287 323 BY SIP DISULFID 287 323 BY SIP DISULFID 297 325 BY SIP DISULFID 297 325 BY SIP DISULFID 297 329 BY SIP
                                                                                                                                                                                                                                                                                                                                              EMBL; U83916; AAC48756.1; -.
InterPro; IPR000359; -.
InterPro; IPR000867; -.
InterPro; IPR000884; -.
InterPro; IPR001007; -.
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Best Local Similarity 97.1%;
Matches 165; Conservative '
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Pfam; PF00219; IGFBP; 1.
Pfam; PF00090; tsp_1; 1.
Pfam; PF00093; vwc; 1.
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256
3
256
273
384
387
349 AA;
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P29268;
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CTGF_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRIT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97390475; PubMed=9242708;
MEDLINE=97390475; PubMed=9242708;
Brigstock D.R., Steffen C.L., Kim G.Y., Vegunta R.K., Diehl J.R.,
Harding P.A.;
"Purification and characterization of novel heparin-binding growth
factors in uterine secretory fluids. Identification as heparin-
fluids. Identif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Sus scrofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Cetartiodactyla; Suina; Suidae; Sus.
Mammalia; Eutheria; Cetartiodactyla;
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BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

MISSING (IN SHORT ISOFORM).

MISSING (IN SHORT ISOFORM).
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 948; DB 1; Length 349; 100.0%; Pred. No. 1.1e-77; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 TLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRRWYGDMA 349
                                                                                                                                                                                                                                                                                                                                                                                                                  CONNECTIVE TISSUE GROWTH FACTOR
                                                                                                                                                                                                                    pfam; pF0007; Cy2,Knot; 1.
pfam; pF0019; IGFBP; 1.
pfam; pF00039; tsp_1; 1.
prosite; P500222; IGF_BINDING; 1.
pROSITE; P500185; CTCK_1; 1.
pROSITE; P501208; VWFC; 1.
PROSITE; P501208; VWFC; 1.
PROSITE; P501208; VWFC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 170; Conservative
                                                   M92934; AAA91279.1;
X78947; CAA55544.1;
                                                                                                                                                min; izivo,
Interpro; IPR000359; -.
Interpro; IPR000867; -.
Interpro; IPR000884; -.
Interpro; IPR001007; -.
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                                                                                           PIR; A40551; A40551.
PIR; S44205; S44205.
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                                                                                                                                      MIM; 121009;
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019113;
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CTGF_PIG
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Gaps

Length 349;

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121 TLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 170
                                                                                                        CTGF_BOVIN
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                                                                           KESULT 4
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                                 299
                                                                                                                                                                                                          Bos
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                              QQ
                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                   DNA CELL BLOL. 10:293-300(1991).

--- TISSUE SPECIFICITY: TESTIS, SPLEEN, KIDNEY, LUNG, HEART, AND BRAIN (LOWEST LEVEL IN TESTIS AND HIGHEST IN LUNG).

--- INDUCTION: BY GROWTH FACTORS.

--- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN FAMILY. CEF-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.

--- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                               SEQUENCE FROM N.A. MEDLINE-91229699; PubMed-2029337; Brunner A., Chinn J., Neubauer M.G., Purchio A.F.; Identification of a gene family regulated by transforming growth
                                           Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;
"Structure, mapping, and expression of fisp-12, a growth factor-
inducible gene encoding a secreted cysteine-rich protein.";
Cell Growth Differ. 2:225-233(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 926; DB 1; Length 348;
Pred. No. 9.7e-76;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> E (IN REF. 2).
735B65B6A711686F CRC64;
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE: PS00222; IGF_BINDING; 1. PROSITE: PS01185; CTCK_1; 1. PROSITE: PS01225; CTCK_2; 1. PROSITE: PS01208; VWFC; 1. Growth factor binding; Signal. 25 Growth 26 348 CONNEC CHAIN
[1]
SEQUENCE FROM N.A.
MEDLINE-91363290; Pubmed-1888698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 B3
161 K
37793 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M70641; AAA37627.1; -.
EMBL; M70642; AAA37628.1; -.
EMBL; M80263; AAA73135.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.78;
95.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001007; --
Pfam; PF00007; Cys_knot; 1.
Pfam; PF00219; IGFBP; 1.
Pfam; PF00090; tsp_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.7
Best Local Similarity 95.9
Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A53228; A53228.
MGD; MGI:95537; F1sp12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000359; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000884; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291
161
348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000867
                                                                                                                                                                          factor-beta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONNECTIVE TISSUE GROWTH FACTOR VWFC.
Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
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9; D919023AE40D212E CRC64;
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1larity 96.5%; Pred. No. 5.9e-74;
Conservative 2; Mismatches 4;
                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CONNECȚIVE TISSUE GROWTH FACTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00222; IGF_BINDING; FALSE_NEG.
PROSITE; PS01185; CTCK_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01225; CTCK_2; 1.
PROSIȚE; PS01208; VWFC; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CICK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF000137; AAB66596.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38152 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Growth factor binding; Signal SIGNAL 1 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001007; -.
Pfam; PF00007; Cys_knot; 1.
Pfam; PF00219; IGFBP; 1.
                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00090; tsp_1; 1.
Pfam; PF00093; vwc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000867; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000884; -.
                                                                                                                                                                                              Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000359;
                                                                                                                                                           taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                             NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         349
                                                                                                                                                                                                                                                TISSUE=Aorta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120

61

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Gaps

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40; Indels

22; Mismatches

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94;
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P28686;
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  Matches
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                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordatà; Craniatà; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                        61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
                                   180 AAYRLEDTFGPDPTMIRANCQVQTTEWSAYSKTCGMGISTRVTNDNAFCRLEKQSRLCMV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCK.

BY SIMILARITY.

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BY SIMILARITY.

N. LINKED (GLONAC. ..) (POTENTIAL).

W, 717D9F8533882E89 CRC64;
                                                                  binding; Signal.
                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
NOV PROTEIN PRECURSOR.
                                                                                                                                                                                                                        Coturnix coturnix japonica (Japanese quail).
                                                                                                                                                353 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
NOV PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00222; IGF_BINDING; 1.
PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01208; VWFC; 1.
PROSITE; PS01208; VWFC; 1.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38667 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U13063; AAA21128.1; -.
InterPro; IPR000359; -.
InterPro; IPR000867; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00007; Cys_knot; 1.
Pfam; PF00219; IGFBP; 1.
Pfam; PF00090; tsp_1; 1.
                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000884; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001007; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 AA;
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      NCBI_TaxID-93934;
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                                                                                                                                         V_COTJA
NOV_COTJA
P42642;
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                                                                                                                                                                                                                                                               Coturnix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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Score 541.5; DB 1; Length 353; Pred. No. 1.8e-41;

57.18; 59.98;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONTOUR V., MAILLIBLIE C. COMMINION OF A COLOCHE J. PERDAI B.;
COOCHE J. V. PERDAI B.;
COOCHE J. COO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN FAMILY. CEF-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.
--- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
--- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoštomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                               61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
                                                                                                                                                                                 185 AAYRQEATLGIDVSDSSANCIEQTTEWSACSRSCGMGFSTRVTNRNQQCEMVKQTRLCMM 244
                                 1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKGSRLCMV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92107157; PubMed=1309586;
Joliot V., Martinerie C., Dambrine G., Plassiart G., Brisac M.,
                                                                                                                                                                                                                                                                       121 TLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIF 157
                                                                                                                                                                                                                                                                                                            01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X59284; CAA41975.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR000359; ...
Interpro; IPR000867; ...
Interpro; IPR000884; ...
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOV PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=BROWN LEGHORN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus.
NCBI_TaxID=9031;
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InterPro; IPR000867;
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           ODR WORK WENT THE FET 
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Gene 17:1243-248(199);

-1-71:243-248(199);

-1-FUNCTION: IMMEDIATE-BERLY PROTEIN LIKELY TO PLAY A ROLE IN CELL GROWTH REGULATION (BY SIMILARITY).

-1-SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN FAMILY. CEF-10/CYRGI/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.

-1-SIMILARITY: CONTAINS 1 VWFC DOMAIN.

-1-SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96257227; PubMed-8666280;
Ying Z., King M.L.;
"Isolation and characterization of xnov, a Xenopus laevis ortholog of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL)
1ECB3FA3058C6797 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.0%; Score 540.5; DB 1; Length 351; 59.9%; Pred. No. 2.3e-41; Live 22; Mismatches 40; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS01185; CTCK_1; 1.
PS01225; CTCK_2; 1.
PS01208; VWFC; 1.
cogene; Growth factor binding; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 AA.
                                                                                                                                                                                                                                            VWFC.
CTCK.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                      NOV PROTEIN.
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IGF_BINDING; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38268 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U37063; AAB17096.1; -. InterPro; IPR000359; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 59.94
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae; Xenopus.
NCBI_TaxID-8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                   Proto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOV_XENLA
P51609;
                                                                                                                                                                                                                                                                                     DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                    PROSITE;
                                                                                                           PROSITE
                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                          CHAIN
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NOV_XENLA

NOV_XENLA

NOV_XENLA

DT 01-0C

DT 
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STROMAL TYPE.

-:- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN FAMILY.

-:- SIMILARITY: CONTAINS 1 VWFC DOMAIN.

-:- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPCEADLEENI-KKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Martinerie C., Huff V., Joubert I., Badzioch M., Saunders G.,
Strong L., Perbal B.;
"Structural analysis of the human nov proto-oncogene and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oncogene 9:2729-2732(1994).
-!- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GROWTH REGULATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL).
677D7078EB21365F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                                                                                                                                                                                                                                                                                         Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                   POTENTIAL.
NOV PROTEIN HOMOLOG.
VWFC.
CTCK.
                                                                                                                                                                                                                                                                                                                                                                         54.7%; Score 518.5; DB 1; 57.2%; Pred. No. 2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                       45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 TTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFE 158
                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 2e-39;
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 AA
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NOV PROTEIN HOMOLOG PRECURSOR (NOVH)
                                                                                       PROSITE; PS00222; IGF_BINDING; 1.
PROSITE; PS01208; WWFC; 1.
PROSITE; PS01185; CTCK_1; FALSE_NEG.
PROSITE; PS01225; CTCK_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-94336229; PubMed-7520150;
                                                                                                                                                    Growth factor binding; Signal.
                                                                                                                                                                                                                                                                                                                             38070 MW;
                              Pfam; PF00007; Cys_knot; 1.
Pfam; PF00219; IGFBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                          PF00090; tsp_1; 1.
IPR000884;
IPR001007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 91; Conserv
                                                                            Pfam; PF00093; vwc;
                                                                                                                                                                                                                                                                                                                           343 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in Wilms tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOV_HUMAN
P48745:
 InterPro;
              InterPro;
                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                 DISULFID
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                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                   DOMAIN
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                                                             Pfam;
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STRAIN-129/SV, AND ICR; TISSUE-Brain;
MEDLINE-97131523; PubMed-8975721;
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354 AA;
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                                                                                                                          [2]
SEQUENCE FROM N.A.
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Best Local Si
Matches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
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              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RPCEADLEE-NIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 AAYRPEATLGVEVSDSSVNCIEOTTEWTAGSKSCGMGFSTRVTNRNRQCEMLKOTRLCMV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AAYRLEDIFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRYTNDNASCRLEKQSRLCMV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
035D5BF4576BD85B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.3%; Score 515; DB 1; Length 357;
ilarity 54.4%; Pred. No. 4.3e-39;
Conservative 25; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN HOMOLOG
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NOV_MOUSE STANDARD: PRT; 354 AA.
NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1907 (Rel. 39, Last annotation update)
NOV PROTEIN HOMOLOG PRECURSOR (NOVH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VWFC.
CTCK.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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                                                                                                                                                                            EMBL, X78351, CAA55146.1; --
EMBL, X78352, CAA55146.1; JOINED.
EMBL, X78353, CAA55146.1; JOINED.
EMBL, X78354, CAA55146.1; JOINED.
EMBL, X96584; CAA65403.1; --
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                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001007; -.
Pfam; PF00007; Cys_Knot; 1.
Pfam; PF00219; IGFBP; 1.
Pfam; PF00090; tsp_1; 1.
Pfam; PF00099; vwc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39162
                                                                                                                                                                                                                                                                                          Interpro; IPR000359; --
Interpro; IPR000867; --
Interpro; IPR000884; --
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357 AA;
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                                                                                                                                                                                                                                                                                  MIM; 164958; -
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CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                             nephrogenesis."
oncogenesis."
oncogenesis.
oncogenesis.
-1-4192(1996).
-1-5UNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
GROWTH REGULATION (BY SIMILARITY).
-1-5UNCTION: THE INSULIN-LIKE GROWTH FACTOR BINDING
-1-5THALARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
-1-5THALARITY: CONTAINS 1 VWFC DOMAIN.
-1-5IMILARITY: CONTAINS 1 VWFC DOMAIN CYSTINE KNOT-LIKE DOMAIN (CTCK).
-1-5IMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCK.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N.LINKED (GLCHAC. ...) (POTENTIAL).

N.LINKED (GLCHAC. ...) (POTENTIAL).

N.LINKED (GLCHAC. ...) (POTENTIAL).

N.LINKED (GLCHAC. ...)
Snaith M.R., Natarajan D., Taylor L.B., Choi C.P., Martinerie C., Eprbal B., Schofield P.N., Boulter C.A.; "Genomic structure and chromosomal mapping of the mouse nov gene."; Genomics 38:425-428(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
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                                                                                                                                                                                                                      STRAIN=C57BL/6;
MEDLINE=9852204003; PubMed-8622864;
MEDLINE=96204003; PubMed-8622864;
MAILINE-16 C., Chevaller G., Rauscher F.J. III, Perbal B.;
"Regulation of nov by WI1: a potential role for nov in
"Regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOV PROTEIN HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binding; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00222; IGE_BINDING; 1. PROSITE; PS01185; CTCK_1; 1. PROSITE; PS01285; CTCK_2; 1. PROSITE; PS01228; VWFC; 1. Proto-oncogene; Growth factor bin Proto-oncogene; Growth factor bin Proto-oncogene; Growth factor bin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Μ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; x97863; CAA66457.1; --
EMBL; x96255; CAA70454.1; --
EMBL; x96585; CAA65404.1; --
MGD; MGI:109185; Nov.
InterPro; IPR000859; --
InterPro; IPR000867; --
InterPro; IPR000884; --
InterPro; IPR001007; --
Pfam; PF00007; Cys_knot; 1.
Pfam; PF00009; LSPBP; 1.
Pfam; PF00009; LSPBP; 1.
Pfam; PF00099; LSPBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38928
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CYR6_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/ r send an email to license@isb.ch).
                                                                                                                                                                                                                                                                                                                                        -1- DEVELOPMENTAL STAGE: EXPRESSED FROM G(0)/G(1) THROUGH MID-G(1) IN NORMAL CELLS, AND AT A CONSTANT LEVEL IN RAPIDLY GROWING CELLS.
-1- INDUCTION: BY GROWTH FACTORS.
-1- SINILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING PROFEIN FAMILY. CEF-10/CXR61/CTFG/FISP-12/NOV PROFEIN SUBFAMILY.
-1- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
-1- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                          O'Brien T.P., Yang G.P., Sanders L., Lau L.F.;
"Expression of cyr61, a growth factor-inducible immediate-early
gene.";
|: |||:| ||:|| || ||:|| 311
                                                                                                  01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CYR61 PROTEIN PRECURSOR (3CH61).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
CYR61 PROTEIN.
                                                                             379 AA
                                                                                                                                                                                                                                                                                                                  Mol. Cell. Biol. 10:3569-3577(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001007; -.
Pfam; PP00007; Cy2_knot; 1.
Pfam; PP00019; tGPBP; 1.
Pfam; PP00099; wcv; 1.
PROSITE; PS00222; IGF_BINDING; 1.
PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01203; WWFC; 1.
PROSITE; PS01203; WWFC; 1.
Growth factor binding; Signal.
                                                                             PRT;
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Fibroblast;
MEDLINE-90287146; PubMed-2355916;
O'Brien T.P., Yang G.P., Sanders I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M32490; AAA37512.1; -.
EMBL; X56790; CAA40109.1; -.
PIR; A35689, A35689.
MGD; MGI:88613; Cyf.1.
InterPro; IPR000359; -.
InterPro; IPR000867; -.
                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000884; -.
                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                         CYR61 OR IGFBP10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IN LUNG.
                                                                            CYR6_MOUSE
P18406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                  RESULT 10
CYR6_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Albrecht C., von der Kammer H., Klaudiny J., Mayhaus M., Nitsch R.M.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 PCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTT 121
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               9 FGPDPTMI-----RANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The human growth factor-inducible immediate early gene, CYR61, maps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    000622; 014934;
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CYR61 PROTEIN PRECURSOR (GIG1 PROTEIN) (INSULIN-LIKE GROWTH FACTOR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jay P., Berge-Lefranc J.L., Marsollier C., Mejean C., Taviaux S., Berta P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEINS; PROMOTES PROLIFERATION, MIGRATION AND ADHESION (BY
                                                                                                                                                                                                                                                                                                                                                                         ٠<u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bi A.B., Yu L.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY ACT AS ONE OF THE MANY GROWTH FACTOR-BINDING
                                                                                                                                                                                                                                                                                                          Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 LPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDM 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 VKMRFRCEDGEMFSKNVMIQSCKCNYNCPHPNEASFRLY--SLFNDI 374
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kolesnikova T.V., Lau L.F.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                    FA6B5014B56A8EE9 CRC64;
                                                                                                                                                                                                                                                                                                          51.4%; Score 487.5; DB 1;
49.4%; Pred. No. 1.3e-36;
tive 32; Mismatches 44;
                         CTCK.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

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BY SIMILARITY.
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MEDLINE=97280750; PubMed=9135077;
                                                                                                                                                                                                                    MΝ.
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                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 49.48
                                                                                                                                                                                                                 41709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING PROTEIN 10).
CYR61 OR IGFBP10 OR GIG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
   164
358
321
335
351
353
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98
284
284
301
312
315
320
379 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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   DOMAIN
DOMAIN
DISULFID
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SEQUENCE
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Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianiae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTTLPVE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
NECHTURIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPHA) (GDNF RECEPTOR BETA) (GDNFR-BETA).
GFRAZ OR GDNFRB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGPDP---TMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEA 65
                     -!- FUNCTION: PROBABLE SECRETED REGULATOR FROM PROTOR BINDING
-!- INDUCTION: BY V-SRC.
-!- SIMILARITY: BELOW.
-!- SIMILARITY: CEF-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.
-!- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
-!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 50.6%; Score 479.5; DB 1; Length 375; Best Local Similarity 51.3%; Pred. No. 6.5e-36; Matches 81; Conservative 27; Mismatches 45; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCK.
BY SIMILARITY.
W, 95F28553BE35D5AE CRC64;
PROBABLE SECRETED REGULATORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 FKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CEF-10 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A4L14C; A712C;
InterPro; 1PR000867; -
InterPro; 1PR000867; -
InterPro; 1PR000884; -
InterPro; 1PR001007; -
Pfam; PF00007; Cys_knot; 1.
Pfam; PF00090; LGFBP; 1.
Pfam; PF00090; LGFBP; 1.
PROSITE; PS00122; LGF_BINING; 1.
PROSITE; PS01225; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01208; VWFC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J04496; AAA48661.1; -.
PIR; A41428; A41428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40651
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013157;
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DISULFID
SEQUENCE
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                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 EADLEENIKKKKKKIRPRISKPIKPELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTTLP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : ::|||||| :| :|::| :|| :|::| :|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 VEFKCPDGEVMKKNNMFIKTCACHYNCPGDNDIFESLYYRKMYGDM 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333 MRFRCEDGETFSKNVMMIQSCKCNYNCPHANEAAFPFY--RLENDI 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> I (IN REF. 4).
-> R (IN REF. 4).
FC0BD39C078CA0B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.2%; Score 485.5; DB 1;
50.0%; Pred. No. 1.9e-36;
tive 29; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOT-1996 (Rel. 34, Last annotation update)
CEF-10 PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSO0222; IGF_BINDING; 1. PROSITE; PSO1185; CTCK_1; 1. PROSITE; PSO11225; CTCK_2; 1. PROSITE; PSO1225; CTCK_2; 1. PROSITE; PSO1208; VWFC; 1.
                                                                                                                                                                               EMBL: Y12084; CAA72802.1; EMBL: U62015; AAB58319.1; EMBL: AF003594; AAB61240.1; EMBL: A6031985; AAB61247.1; Interpro: IPR0000867; Interpro: IPR000867; Interpro: IPR000867; Interpro: IPR000087; Ffam; PF00209; Interpro: IPR001007; Pfam; PF00209; Yed: Interpro: IPR001007; Pfam; PF00009; Yed: Interpro: IPR001007; Pfam; PF00009; Yed: Interpro: IPR001007; Pfam; PF00009; Yed: Interpro: IPR00109; Yed:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42026 MW;
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P19336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83;
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Best Local Si
Matches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DISULFID
DISULFID
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FSPO_XENLA
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CARBOHYD
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                                                                                                                                           SUBCELULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
SIMILARITY: BELONGS TO THE GDNFR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                              175 LRSGYISTC----SKEISATEHCSRR-KCHKALRQFFDNVPSEYTYRLIFCS-CKDQACA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 TPHRTTTLPVEFKCPDGEVMKKNMM--------FIKTCACHY----NCPG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 EPRROTIVPF---CSYEDKEKPNCLDLRNVCRADHLCRSRLADFHANCQASFQSLTSCPG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 RLSDIFRLASIFSGMDPATNSKSNHCL------DAAKACNL-----NDNC-----KR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 SRLCMVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCC 114
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                              4 RLEDTF------GPDP-TMIRAN-CLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQ 54
                                                                                                                                                                                                                                                                                                        HYDROPHOBIC, REMOVED DURING MATURATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                         :65
                                                                                                                                                                                                                                                                                                                                                                                                   10.7%; Score 101.5; DB 1; Length 465; 25.8%; Pred. No. 0.039; live 15; Mismatches 61; Indels 59
                                                                                                                                                                                                                                                                                                                                                          GPI-ANCHOR (POTENTIAL).
22CD9024ED971F06 CRC64;
                                                                                                                                                                                                                                                                                   POTENTIAL.
NEURTURIN RECEPTOR ALPHA
                                                                                                                                                                                                                                                             EMBL; U90542; AAB61571.1; -.
Receptor; Glycoprotein; GPI-anchor; Membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-CTT-2000 (Rel. 40, Last annotation update)
F-SPONDIN PRECURSOR.
                                        MEDLINE-97336104; PubMed-9192899;
                                                                                                                                                                                                                                                                                                                                                                       51908 MW;
                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 25.8%
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                412
                                                                                                                                                                                                                                                                                                        465
                                                                                                                                                                                                                                                                                                                            355
387
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387
412
445
465 AA;
                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                             22
446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 DN 154
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P35446;
                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                  -I- FUNCTION: PROMOTES THE ATTACHMENT OF SPINAL CORD AND SENSORY NEURON CELLS AND THE OUTCROWTH OF NEURINES IN VITRO, MAY CONTRIBUTE TO THE GROWTH AND GUIDANCE OF AXONS IN BOTH THE SPINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------ADLEENIKKGKKCIRTPKISKPIKFELSG 93
                                                                                                                                                                                                                                                                             -:- SUBCELLULAR LOCATION: SECRETED.
-:- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE FLOOR PLATE.
-:- SIMILARITY: CONTAINS 6 TYPE-1 TSP DOMAINS.
                                             Klar A., Baldassare M., Jessell T.M.; "F-spondin: a gene expressed at high levels in the floor plate encodes a secreted protein that promotes neural cell adhesion and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.7%; Score 101.5; DB 1; Length 807; 24.7%; Pred. No. 0.065; artive 19; Mismatches 46; Indels 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 CISMKTYRAKFCGVCTDGRCCTPH-.RTTTLPVE----FKCPDGEVMKK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JANNED (GLCNAC. . .) (P. 309525F9EAFEA89A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
F-SPONDIN.
TSP TYPE-1 1.
TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 4.
TSP TYPE-1 4.
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TISSUE=Embryonic floor plate;
MEDLINE=92208952; PubMed=1555244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90773 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M88469; AAA41174.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR, A8152; A38152.
InterPro; IPR000884; -
InterPro; IPR000881; -
Pfam; PF02014; Reeler; 1.
Pfam; PF00090; tsp_1; 6.
PROSITE; PS50092; TSP1; 5.
Glycoprotein; Signal; Repeal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae; Xenopus
                                                                                                                          neurite extension.";
Cell 69:95-110(1992)
                                                                                                                                                                                                                                                           CORD AND THE PNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F-SPONDIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SC SC DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 IKKGKKCIRTPKISKPIKFELSGCTSMKTYRA-----KFCGVCTDGRCCTPHRTTTLPVE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 LVQTTEWSACSKTCGMG--ISTRVTN-----DNASCRLEKQSRLCMVRPCE---ADLEEN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 26.8%; Pred. No. 0.11;
Matches 38; Conservative 18; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                -LINKED (GLCNAC. . .) (P. D3A54E329548AED9 CRC64;
                                                                                                                                                                                                                                                                                                                                           Cell adhesion.
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TSP TYPE-1 1.
TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 5.
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                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         787 TSCKD----KKE---IRACNVH 801
                                   TISSUE=Embryo;
MEDLINE=93376785; PubMed=8367492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               90702 MW;
                                                                                                                                                                                                                                                                     EMBL; L09123; AAA19105.1; -.
                                                                                                                                                                                                                                                                                       InterPro; IPR000884; -.
InterPro; IPR002861; -.
Pfam, PF02014; Reeler; 1.
Pfam, PF00090; tsp_1; 6.
PROSITE; PS50092; TSP1; 6
                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Signal SIGNAL
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803 AA;
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                       SEQUENCE FROM N.A.
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09z0g4 mus musculu 09jhc6 rattus norv Q9ud16 homo sapien Q19791 caenorhabdi Q9w493 drosophila

097574 bos taurus 076076 homo sapien drosophila bos taurus

Q9pss6 gallus gall Q17591 caenorhabdi Q0261 bos taurus Q23729 cryptospori Q25757 plasmodium Q97467 plasmodium Q9428 homo sapien Q9hcb6 homo sapien Q4113 brachydanio Q9uf31 drosophila Q9uft0 drosophila Q9tt0 drosophila

Q9gxt7 mus musculu Q43384 homo sapien Q9upz6 homo sapien Q9npm2 homo sapien Q19pm2 capien Q19284 caenorhabdi

O9npm2 homo sapien O19284 caenorhabdi O9ufz4 homo sapien

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Harding P.A., Brigstock D.R.; "Cloning and sequencing of a porcine connective tissue growth factor (CTGF) chara.".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 98.6%; Score 935; DB 6; Length 34 Best Local Similarity 97.6%; Pred. No. 8.2e-93; Matches 166; Conservative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases EMBL; U70060; AAD00174.1; ... InterPro; IPR000359; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 AA; 37946 MW; 35AB4275AC1D4B3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
U-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CONNECTIVE TISSUE GROWTH FACTOR.
                                                                                                                                                                                                                                                                                           023729
025757
097267
095428
0994CB6
042113
0990631
0990710
043981
099VVK0
097574
076076
092064
091016
019791
099493
09PSS6
017591
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Q19284
Q9UFZ4
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PROSITE; PSO11225; CTCK_2; 1.
PROSITE; PSO1225; IGF_BINDING; 1.
PROSITE; PSO1208; VWFC; 1.
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Best Local Similarity
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09ex72 rattus norv
09wtm9 rattus norv
043775 homo sapien
054775 mus musculu
05958 homo sapien
095389 homo sapien
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09wvs1 rattus norv
09rie9 rattus norv
042607 xenopus lae
09pt80 notophthalm
09z164 rattus norv
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O95388 homo sapien
Q9df21 scyliorhinu
Q9r2c0 rattus norv
                                                                                                                                                                                                            (without alignments)
240.555 Million cell updates/sec
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homo sapien
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                                                                                                                                                                                                                                                                                                                    948
1 AAVRLEDTEGPDPTMIRANC......PGDNDIFESLYYRKMYGDMA 170
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                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                        US-09-461-646-2_COPY_180_349
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                OM protein – protein search, using sw model
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Q43775
Q54775
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Q95389
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Gapop 10.0 , Gapext 0.5
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09WLE9
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_unclassified:*
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sp_phage:*
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sp_bacteria:*
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Maximum DB seq length: 200000000
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Length 349;

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InterPro; IPR000867
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                                                                                                                                                            al Similarity
163; Conserv
                                                                                                                            347 AA;
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SEQUENCE 347 A
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                   SMART; SM00041;
SEQUENCE 347 P
                                                                                                                                                       Query Match
Best Local S:
Matches 163,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                           239
                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 Mathahs M., Schwitters C., Hove M., Rupp S., Erondu N.E.;
"Bovine connective tissue growth factor, organization of th chromosomal gene and demonstration of promoter activity.", submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF309555; AAG30290.1;
                                                                                                                                                                                                                                                                                                                                              Length 349;
                                                                Query Match 98.1%; Score 930; DB 6; Length 34 Best Local Similarity 98.2%; Pred. No. 2.8e-92; Matches 167; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Tezuka K., Tamatani T.;
"Rattus norvegicus connective tissue growth factor.";
"Rattus norvegicus connective EMBL/GenBank/DDBJ databases.
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB0230668; BAA82125.1;
InterPro; IPR000072;
                                                                                                                                                                                                                                                                                                                     349 AA; 37924 MW; 5FFC8EE83EFB4F99 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 16, Last annotation update)
CONNECTIVE TISSUE GROWTH FACTOR.
                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 AA
                                                                                                                                    PRT; 349 AA
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                                                                                                                                      PRELIMINARY;
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TISSUE=LIVER;
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Q9WVS1
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09GL71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CONNECTIVE TISSUE GROWTH FACTOR.
Extrus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                      61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 TLPVEFKCPDGEIMKKNMMFIKTCACHYNCPGDNDIFESLYYRKWYGDMA 347
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                                                                                                                                                                                                                                                                                    6A69511DE72FBF1C CRC64;
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Pred. No. 7.6e-92;
5; Mismatches 2;
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Pred. No. 7.6e-92;
5; Mismatches 2;
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PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00222; IGF_BINDING; 1.
PROSITE; PS01208; VWFC; 1.
Interpro; IPR000359; -.
Interpro; IPR000857; -.
Interpro; IPR000867; -.
Interpro; IPR001007; -.
Pfam; PF00007; -Cys_knot; 1.
Pfam; PF00009; cys_knot; 1.
Pfam; PF00191; IGFBP; 1.
ProDom; PD001629; -; 1.
PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01185; CTCK_2; 1.
PROSITE; PS01285; CTCK_2; 1.
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Pfam; PF00007; Cys.knot; 1.
Pfam; PF00009; tsp_1; 1.
Pfam; PF00093; vwc; 1.
Pfam; PF00219; IGFBP; 1.
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Best Local Similarity 95.9%;
Matches 163; Conservative
                                                                                                                                                                                                                                                                                           37837 MW;
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"Suppression subtractive hybridization identifies high glucose levels as a stimulus for expression of connective tissue growth factor and other genes in human mesangial cells.";
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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MEDLINE-99150373; Pubmed-10026205;
Murphy M., Godson C., Cannon S., Kato S., Mackenzie H.S., Martin F.,
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-RORGELIMB BLASTEMA;
MEDILINE-99033008; PubMed=9813273;
Cash D.E., Gates P.B., Imokawa Y., Brockes J.P.;
"Identification of newt connective tissue growth factor as a target retinoid regulation in limb blastenal cells.";
Gene 222:119-124(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AAYRLEDIFGPDPTMIRANCLVQTIEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMV 60
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
Notophthalmus.
                 Notophthalmus viridescens (Eastern newt) (Triturus viridescens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.4%; Score 885; DB 13; Length 347;
llarity 91.2%; Pred. No. 2e-87;
Conservative 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
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01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
CONNECTIVE TISSUE GROWTH FACTOR (FRAGMENT).
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PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00222; IGF_BINDING; 1.
PROSITE; PS01208; VWFC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ271167; CAB65965.1;
InterPro; IPR000359; -.
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Pfam; PF00090; tsp_1; 1.
Pfam; PF00093; vwc; 1.
Pfam; PF00219; IGFBP; 1.
                                                                                                                            SEQUENCE FROM N.A.
TISSUE=FORELIMB BLASTEMA;
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                                                                                      NCBI_TaxID=8316;
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Matches 155;
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Q9Z164;
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         235 PCEADLEENIKKGKKCIRIPKISKPVKFEFSGCTSVKTYRAKFCGVCTDGRCCTPHRIAT 294
                                                                                                        62 PCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTT 121
                                                                                  61 RPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT
                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CONNECTIVE ISSUE GROWTH FACTOR XCTGF.
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                             121 TLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 170
                                                                                                                                                                                 298 TLPVEFKCPDGEIMKKNWMFIKTCACHYNCPGDNDIFESLYYRKMYGDWA 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Ying Z., King M.L.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93F221C5DB565A81 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                343 AA
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01-MAY-2000 (TIEMBLrel. 13, Crea
01-MAY-2000 (TIEMBLrel. 13, Last
01-MAR-2001 (TIEMBLrel. 16, Last
CONNECTIVE TISSUE GROWTH FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37966 MW;
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Pfam; PF00007; Cys_knot; 1.
Pfam; PF00090; tsp_1; 1.
Pfam; PF00093; vwc; 1.
Pfam; PF000219; IGFBP; 1.
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NCBI_TaxID=8355;
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SEQUENCE 343 AA;
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SEQUENCE FROM N.A.
TISSUE-LUNG, AND PLACENTA;
MEDLINE-20435857; PubMed-10852911;
Albrecht C., von Der Kammer H., Mayhaus M., Klaudiny J., Schweizer M.,
Nitsch R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 PCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                   Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutharya; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10116;
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242 PCEQEPGEATDMKGKKCLRTKKSLKSIHLQFKNCTSLYTYKPRFCGICSDGRCCTPFNTK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Muscarinic acetylcholine receptors induce the expression of the immediate early growth regulatory gene CYR61."; J. Blol. Chem. 275:28929-28936(2000).

EMBL: AF218568; AAG14964.1; - SEQUENCE 379 AA; 41687 MW; 62BF0BBA4C5AFDE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 11; Length 379;
                                     122 LPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDM 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329 VKMRFRCEDGEMFSKNVMIQSCKCNYNCPHPNEASFRLX--SLENDI 374
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UNOKI H., YODORKURA H., FULUKAWA K., YAMAMOLO H.;
UNOKI H., YODORKURA H., FULUKAWA K., YAMAMOLO H.;
UNDMITCHED MRNA.;
SUBDMITCHED MRNA.;
EMBL; AB015877; BAA78339.1; -.
INTEFPC; IPRO00853; -.
INTEFPC; IPRO00864; -.
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Last annotation update)
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Last sequence update)
Last annotation update)
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49.4%; Pred. No. 8.5e-45;
tive 33; Mismatches 43.
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01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, CYSTEINE-RICH PROTEIN 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 49.4%;
Matches 83; Conservative
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Q9ES72;
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Q9ES72
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STRAIN-SPRAGUE-DAWLEY;

KA MEDLINE-20035752; PubMed=10570975;

KA Liu X.-J., Crowe P.D., Kelner G.S., Fan J., Barry G., Manu F.,

Ling N., De Souza E.B., Maki R.A.;

Ling N., De Souza E.B., Maki R.A.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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53.5%: Pred. No. 7.5e-46;
Live 26; Mismatches 51; Indels
                                                                                                                                                                                                                            Length 113;
                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                     113 AA; 12767 MW; 23EA69FC0A60635E CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                          Score 566; DB 11;
Pred. No. 1.5e-53;
4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351
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PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00222; IGF_BINDING; 1.
PROSITE; PS01208; VWFC; UNKNOWN_1.
                       J. Biol. Chem. 274:5830-5834(1999).
EMBL: AF079531; AAD02838.1; ..
InterPro; IPR000359; ..
Pfam. PF00007; Cys_knot; 1.
SMART; SM00041; CT; 1.
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                                                                                                                                                                                                                                Query Match 59.7%;
Best Local Similarity 93.5%;
Matches 101; Conservative
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Best Local Similarity 53.5%
Matches 91; Conservative
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SEQUENCE 351 A
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Best Local Simi
Matches 68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 PCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 9 FGPDPTMI-----RANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                  51.4%; Score 487.5; DB 11; Length 379; 49.4%; Pred. No. 1.4e-44; Live 32; Mismatches 44; Indels. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.2%; Score 485.5; DB 4; Length 381; 50.0%; Pred. No. 2.3e-44; Indels 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 LPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDM 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 VKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHPNEASFRLY--SLFNDI 374
                                                                                                                                                                                                                                                           D2ABAFD77B84762B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9883CE4886C4B430 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381 AA
                                                                                                                                                                                                                       POTENTIAL. CYR61.
InterPro; IPR001007; -.
Pfam; PF00007; Cys_knot; 1.
Pfam; PF00093; vwc; 1.
Pfam; PF000193; vwc; 1.
Pfam; PF00219; IGFBP; 1.
PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01208; VWFC; 1.
SMART; SM00041; CT; 1.
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PS051TE; PS01225; CTCK_2; 1.
PROSITE; PS00222; IGF_BINDING; 1.
PROSITE; PS01208; VWFC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells from the nervous system.";
Mol. Pathol, 50:310-316(1997).
EMBL; Y11307; CAA72167.1; -
InterPro; IPR000859; -.
InterPro; IPR000884; -.
                                                                                                                                                                                                                                                             41728 MW;
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01-JUN-1998 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
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379 AA;
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SEQUENCE 381 AA;
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Best Local Similarity
Matches 83; Conserva
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99061933; PubMed-9843955; Pebnica D.A., Lawrence D.A., Lee J., Pennica D., Swanson T.A., Welsh J.W., Roy M.A., Lawrence D.A., Lee J., Brush J., Taneyhill L.A., Deuel B., Lew M., Watanabe C., Cohen R.L., Melham M.F., Finley G.G., Quirke P., Goddard A.D., Hillan K.J., Gurney A.L., Botstein D., Levine A.J., Goddard A.D., Hillan K.J., WISP genes are members of the connective tissue growth factor family that are up-regulated in wnt-1-transformed cells and aberrantly Proc. Natl. Acad. Sci. U.S.A. 95:14717-14722(1998).

EMBL, AR004873; BAA249491; ...
                                 13 FGMEPRILYNPLOGGKCIVQTTSWSQCSKTCGTGISTRVTNDNPECRLVKETRICEVRPC 272
                                                                                                                                 64 EADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTTLP 123
                                                                                                                                                               273 GQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVK 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE=98119879; PubMed=9449709;
Hashimoto Y., Shindo-okada N., Tani M., Nagamachi Y., Takeuchi K.,
Shiroishi T., Toma H., Yokota J.;
"Expression of the Elml gene, a novel gene of the CCN (connective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                333 MRFRCEDGETFSKNVMIQSCKCNYNCPHANEAAFPFY--RLFNDI 376
                                                                                                                                                                                                                                                              124 VEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDM 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00041; CT; 1.
FEDITENCE 367 AA; 40702 MW; 3B7C0569EFAB5E96 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          murine melanoma cells.";
J. Exp. Med. 187:289-296(1998).
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InterPro; IPR000359; -.
InterPro; IPR000867; -.
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Lawrence D.A., Lee J nnabe C., Cohen R.L.,

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62 PCEADLEENIK--KGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVR 61
                                                                                                                                                                                                                             TISSUE-BONE MARROW, AND FETAL KIDNEY;

TISSUE-BONE MARROW, AND FETAL KIDNEY;

X MEDLINE-99061933; PubMed-9943955;

X MEDLINE-99061933; PubMed-9943955;

X MEDLINE-99061933; PubMed-9943955;

A mendra D., Swanson T.A., Welsh J.W., Roy M.A., Lawrence D.A., Lee J. Brush J., Taneyhill L.A., Deuel B., Lew M., Watanabe C., Cohen R.L., A melham M.F., Finlay G.G., Quirke P., Goddard A.D., Hillan K.J.,

A milham M.F., Finlay G.G., Quirke P., Goddard A.D., Hillan K.J.,

A milham M.F., Finlay G.G., Quirke P., Goddard A.D., Hillan K.J.,

A milham M.F., Finlay G.G., Quirke P., Goddard A.D., Hillan K.J.,

A milham M.F., Finlay G.G., Quirke P.J.,

That are up-regulated in wnt-1-transformed cells and aberrantly

R proc. Natl. Accd Scl. U.S.A. 95:14717-14722(1998).

R proc. Natl. Accd Scl. U.S.A. 95:14717-14722(1998).

R proc. Natl. Accd Scl. U.S.A. 95:14717-14722(1998).

R proc. PRO00078; Syzknot; 1.

R pfam; PPG00090; tsp_l; 1.

R pfam; PPG00190; tsp_l; 1.

R PROSITE; PSG0122; IGF_BINDING; 1.

R PROSITE; PSG0122; IGF_BINDING; 1.

SQ SEQUENCE 354 AA; 33292 MW; 67F48D0D5C2F5EE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                         Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anding B., Long Y.; "Cloning of a new gene down-regulated in the small-cell tumor embryonal-rhabdomyosarcoma (RMS)."; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF003114; AAF21597.1; -
         Olymar-1999 (TremBirel. 10, Created)
01-Mar-1999 (TremBirel. 10, Last sequence update)
01-Mar-2001 (TremBirel. 16, Last annotation update)
CONNECTIVE TISSUE GROWTH FACTOR RELATED PROTEIN WISP-3.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 TILPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.6%; Score 404; DB 4;
llarity 42.2%; Pred. No. 1.3e-35;
Conservative 37; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-MAR-2001 (TrEMBLrel. 16, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 68; Conservat
                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-KIDNEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Q9UID7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UID7
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 PCDSNILKTIKIPKGKTCQPTFQLSKAEKFVFSGCSSTQSYKPTFCGICLDKRCCIPNKS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 SYKIMPAYRNLPLIWKKKCLVQATKWTPCSRTCGMGISNRVTNENSNCEMRKEKRLCYIQ 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chandrasekharappa S., Wu Z.F., Wang Y.F., Bucana C.D., Root H., Chandrasekharappa S., Strawderman M., Ethier S.P., Merajver S.D.; Chandrasekharappa S., Strawderman M., Ethier S.P., Merajver S.D.; A novel putative IGF-binding, tumor suppressor protein, LIBC, and phenotype."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF145679; AAD31517.1; -. InterPro; IPR0000559; -. InterPro; IPR0000559; -. InterPro; IPR0000567; -. InterPro; IPR0000667; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVR 61
                                            79 RIPKISKPIKFELSGCTSMKTYRAKFCGVCIDGRCCTPHRTTTLPVEFKCPDGEVMKKNM 138
                                                                 275 AVYQPEEATNFTLAGGVSTRTYRPKYGGVCTDNRCCIPYKSKTISVDFQCPEGPGFSRQV 334
215 NCIAYTSPWSPCSTTCGLGISTRISNVNARCWPEQESRLCNLRPCDVDIQLHIKAGKKCL 274
                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DJ142L7.3 (CONNECTIVE TISSUE GROWTH FACTOR (NOV, GIG) LIKE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                      DJ142L7.3 OR LIBC.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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42.6%; Score 404; DB 4; Length 331;
Best Local Similarity 42.2%; Pred. No. 1.2e-35;
Matches 68; Conservative 37; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 AA; 36909 MW; D109C2FDCA1DF549 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 TILPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 KMITIQFDCPNEGSFKWKMLWITSCVCQRNCREPGDIFSEL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 AA.
                                                                                                                                                                                                                                                                                              331 AA.
                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000884; --
Pfam; PF00007; Cys_knot; 1.
Pfam; PF00090; tsp_1; 1.
Pfam; PF00019; IGFBP; 1.
PR0SITE; PS01225; CTCK_2; 1.
PROSITE; PS01225; CTCF_BINDING; 1.
                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                   335 LWINACFCNLSCRNPNDIFADL 356
                                                                                                                                       139 MFIKTCACHYNCPGDNDIFESL 160
                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999) (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-MAMMARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00041; CT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE
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095389
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Gaps

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Length 354; 54; Indels

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DR InterPro; IPR000359; -.

DR InterPro; IPR000867; -.

DR InterPro; IPR000867; -.

DR InterPro; IPR000867; -.

DR InterPro; IPR000007; -.

DR Pfam; PP00009; tsp_1; 1.

DR Pfam; PP00090; tsp_1; 1.

DR Pfam; PP0000; tsp_1; 1.

DR Pfam; PP00000; tsp_
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Search completed: August 20, 2001, 22:55:51 Job time: 561 sec

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